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February 12,

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nucleic search,

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GenCore version (c) 1993 - 2004

Compugen 5.1.6

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

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SUMMARIES

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Pred. No.
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01:54:29 ; Search time 615.146 Seconds (without alignments)
1396.582 Million cell updates/sec REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE ORGANISM RESULT 1
AX350501
LOCUS
DEFINITION
ACCESSION Result იი JOURNAL Score AX350501 Sequence 13 AX350501 AX350501.1 Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 13 25-OCT-2001; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo Homo Query Match sapiens sapiens Length from GI:18616097 (human) 21 bp Patent WO0179561. DВ 99 ϕ 04440 010444400 44444 40 ARU427256
APAH19813
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AJ251176 Phoca vit
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X15947 Dugong dugo
AJ251180 Trichechu
AJ251180 Trichechu
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AJ251107 Micropota
AJ251174 Felis cat
AF337538 Hipposide AJ419805 Description PAT Euteleostomi; Hipposide Nyctimene Rhinoloph 06-FEB-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Springer, M.S.,
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Pteropus
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inger, M.S., Teeling, E.C., Madsen, O.,
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RAQLTREKRFTFVLAVUGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
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_xref="taxon:9606"
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adra2b gene; alpha 2B adrenergic receptor
Rousettus amplexicaudatus (Geoffroy's rousette)
Rousettus amplexicaudatus
Rousettus amplexicaudatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
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Resolution of the early placental mammal radiation using Bayesian
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., de Jong,W.W.
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                                                                                                                                                           aar2B gene; alpha adrenergic receptor; subtype Micropotamogale lamottei (Nimba otter shrew) Micropotamogale lamottei
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Parallel adaptive radiations in two major clades of placental
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cynopterus sphinx (Indian short-nosed fruit bat)
Cynopterus sphinx (
Cynopterus sphinx (
Cynopterus sphinx (
Cynopterus sphinx (
Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
Unpublished
2 (bases 1 to 1156)
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                                                Jong, W.W.
Probing 1the protein
                                                                              van Dijk,M.A.M.,
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Mammalia; Eutheria; Insectivora; Tenrecidae; Potamogalinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="alpha adrenergic receptor 2B"
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LASSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPRAKGGLRDSESKQPHRVPGGPSTL
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EIGEEEDECEPQALPASPASACSPPRQQPQGSRVLATLRGQVLLGKGLGTASGQWWRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="aar2B"
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                                                                                                                                                                                                                                                                                         Nature 409
21082081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      aar2B gene;
Felis catus
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1. .1156
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:1. .>1162
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                                                                                                                                                           ocation/Qualifiers
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                                                                                                                             organism="Felis catus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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Direct Submission
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mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha adrenergic receptor 2B. (cat)
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California, 1354 Speith, Riverside, CA 92521, USA
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Jong, W.W.
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Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;
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ringer,M.S., Teeling,E.C., Madsen,O.,
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LASSIGSFFAPCLIMILYYLRYYLIAAKRSHRAPRAKGRPREGESKQPRPVPTGTSTK
SPEEDAEDESAGGBANGHSKPTGAKEEGETPEDDAIPALPSWSALPNGGQGKKEGVCGA
WWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
394 c 346 g 237 t
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Microbat paraphyly and the convergent evolution of a key innovation in Old World rhinolophoid microbats
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
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Madsen,O.
Direct Submission
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addra2b gene; alpha 2B adrenergic receptor.
Nyctimene albiventer (common tube-nosed fruit bat)
Nyctimene albiventer
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GQWWRRRAQLTREKFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
92 a 378 c 348 g 249 t
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Nijmegen, NETHERLANDS
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Phoca vitulina (harbor seal)
Phoca vitulina
Phoca vitulina
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
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Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
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AJ419806
AJ419806.1 GI:18643973
adra2b gene; alpha 2B adrenergic receptor.
Rhinolophus creaghi
Rhinolophus creaghi
Nature 409 (6820), 610-614 (2001) 21082081 11214318
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Nijmegen, P.O. Box 9101, 6500 HB Nijmegen, NETHERLANDS
Location/Qualifiers
                                                               Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adki
Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                         AJ251176
AJ251176.1 GI:11322419
                                                                                                                                                                                                                                                              PVI251176 1168 Phoca vitulina partial aar2B
                                                      mammals
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Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;
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95 a 391 c 344 g 235 t 2 others
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Emballonuridae;
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Madsen,O.
Direct Submission
Submitted (18-NOV-1999) Madsen O., Department of Biochemistry,
Submitted (Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                                                                                                                   Submitted (17-JAN-2001) Department of Biology, University California, 1354 Speith, Riverside, CA 92521, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taphozous
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                                                                                                                                                                                                     Springer, M.S.,
                                                                                                                                                                                                                                                                                    Integrated fossil and molecular data reconstruct bat echolocation Proc. Natl. Acad. Sci. U.S.A. 98 (11), 6241-6246 (2001)
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ringer.M.S., Teeling,E.C.,
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ilarity 100.0%;
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LPTLASLAASEEANGHSKFFTGEKEGDTPEDDFTPALPFWSALPSSGQSVEGVCGAS
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                                                                                                Location/Qualifiers
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Submitted (15-NOV-1999) O. Madsen, University of Nijmegen,
Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
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3 (bases 1 to 1171)
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Submitted (16-DEC-1997) O. Madsen,
Department of Biochemistry, PO Box
NETHERLANDS
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Highly congruent molecular
of edemic African mammals
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alpha adrenergic receptor; subtype
Dugong dugon (dugong)
Dugong dugon
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Mammalia; Eutheria; Sirenia; Dugongidae; Dugong
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dugon gene encoding alpha
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                                                                                                                                                                                       , 1999 this sequence version replaced gi:3288142.
Location/Qualifiers
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/product="alpha adrenergic receptor
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Pred. No. 18;
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9101, NL-6500 HB Nijmegen,
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TMA251109
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GCTCATCATCCCTTTCTCGCT 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ251109 1 GI:11191771
aar2B gene; alpha adrenergic receptor;
Trichechus manatus (Caribbean manatee)
Trichechus manatus (Caribean manatee)
Bukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Sirenia; Trichechic
                         GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Madsen, O.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probing 1the protein sequence support for the 'African clade' of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Dijk, M.A.M., Madsen, O., Catzeflis, F.,
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                                                                                                                                                                      183
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                                                                                                                                         /codon_start=2
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LSSSIGSFFAPCLIMILVYLRAYLIAKRSHRRGPGAKGAPKKGESKQCHSLDSGPSAL
SSSIGSFFAPCLMILVYLRAYLIAKRSHRRGPGAKGAPKKGESKQCHSLDSGPSAL
ANLPTLASSLAVAGEADGHSMPPGEKKRETSSDDGTPTLPESWGPVLDNSGQOKEGVC
GASLBEBADKEBEBCGPPAVPASPATACSPPLQPPQGSRVLATLRGQVFLGRGVGAA
GASLBEBADKEBEBECGPPAVPASPATACSPPLQPPGSSYSLGAICPQHCRVPHGLF"

83 a 404 c 342 g 242 t
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                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="aar2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DN/db_xref="taxon:9778"
                                                                                                                                                                                                                                                                                                                                                                                     gene="aar2B"
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LSSSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPGAKGGPKKGESKQPHSLDSGPSAL
ANLPTLAASLAVAGEANGHSMPPGEKERETSEDPGTFTLPPSWPVLPNSGQGOKGGVC
GASLEEEADKEEEEECGPPAVPASPATACNPPLQQPOGSQVLATLRGQVFLGRGVGAA
GGQWWRRWAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
a 397 c 337 g 247 t 1 others
                                                                                         100.0%;
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Sirenia; Trichechidae; Trichechus.
                                                                                         Score 21;
Pred. No.
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          AJ427256
AJ427256.1 GI:21655547
AJ427256.1 GI:21655547
A2AB gene; alpha 2B adrenergic receptor.
Aplodontia rufa
Aplodontia rufa
Bukeryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Aplodontidae;
Aplodontia.
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aar28 gene; alpha adrenergic receptor 2B.
Cynocephalus variegatus (Malayan flying lemur)
Cynocephalus variegatus
Cynocephalus variegatus
Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Dermoptera; Cynocephalidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adki
Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYNOCEPHALUS VARIEGATUS partial ear2B
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Aplodontia rufa partial
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21082081
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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GGQWMRRRRAQLSREKRTFTLAVVIGAFVLCWFPFFFSYSLGAICPORCKVPHGLF"
3 a 388 c 369 g 241 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Cynocephalus variegatus"
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141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-JAN-2002) Douzery E.J.P., l'Evolution, Lab. Paleonto., Paleobio., Montpellier II, Pl. E. Bataillon, 34 099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Douzery, E.J.P.
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                                GCTCATCATCCCTTTCTCGCT
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                                                                  Conservative
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SPEEEGEEEEEECDQCDGQSVPASSASVCSPPLQKPQGSRVLATLRGPVLLGRGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/protein_id="CAD20294.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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seq length: 2000000000
N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

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Gapop 10.0 , Gapext 1.0
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21
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Copyright (c) 1993 - 2004
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Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

υναυνο ρω	Result
22222222	Score
100.0 21 100.0 1344 100.0 1344 100.0 1353 100.0 1353 100.0 1353 100.0 1353	Query Match Length DB
13444 13444 135444 1353 1353 2072	Length
22222222	BB
23 AAI99907 22 AAD04761 23 AAI99906 24 AAD44388 22 AAD04762 23 AAI99905 24 AAD44389 25 ACA56583	SUMMARIES
Human alpha-2BAR g Human alpha-2B-adre Human alpha-2BAR t Human alpha-2B-adre Human alpha-2B-adre Human alpha-2B-adr Human alpha-2B-adr	Description

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16.4 16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.8	16.8	16.8	16.8	•	16.8	16.8	16.8	17.8	17.8	18.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	ø	21	21	21
78.1 78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	78.1	٠	80.0	80.0		٠	80.0	80.0	80.0		٠	87.6	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	8	100.0	100.0
1049 1408	1017	1017	1017	958	958	958	958	954	954	954	954	7933	7327	967	401	401	401	376	261	7720	3840	297	7353	7353	3653	3604	2064	2064	1733	1733	1350	1350	6904	6904	3274
22 25	24	24	22	24	24	24	24	24	24	24	22	23	23	21	23	23	23	23	21	23	23	25	24	24	25	25	18	12	24	24	23	23	24	24	25
AAH32040 ABX17873	ABK37708	ABZ43146	AAS42422	ABN89128	ABN89127	ABQ88380	ABT05663	ABK37734	ABN89119	ABN89118	AAS42448	ABL08720	ABL08624 ·	AAA76276	ABV43654	ABV34803	ABV04521	ABV13690	AAC08191	ABL18138	ABL18139	ABX83493	AAD28363	ABL32073	ABZ42623	ACA56582	AAT59499	AAQ14151	ABQ47501	ABQ47500	AAI99918	AAI99917	AAD28365	ABL32075	ABZ42624
Human olfactory re cDNA encoding huma	DNA encoding G-cou	Human GPCR polynuc	Human cDNA encodin	Human GPCR8b nucle	Human GPCR8a nucle	Human G protein co	GPCR 12 protein en	DNA encoding G-cou	Human GPCR4b nucle	Human GPCR4a nucle	 Human cDNA encodin 	Drosophila melanog	Drosophila melanog	Maize glutathione-	Human prostate exp			prostate	Human secreted pro	Drosophila melanog			Human chemically t		Human alpha 2a-adr		Human alpha-2b adr	Human alpha 2 beta		Oligonucleotide fo	Human alpha-2AAR v	alpha-2AAR		Human immune syste	Human alpha 2b-adr

ALIGNMENTS

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RESULT 1
AAL19907
ID AAL19907
XX AAL19907
XX AAL19
XX Huma
XX Huma
XX Huma
XX Phomo
OS Homo
OS Homo
OS Homo
XX WO20
XX YO25-0
XX I 17-A
PR 110-A
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss.
                                                                                                                                                                                                                                         17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha-2BAR genotyping PCR primer SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI99907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI99907 standard; DNA; 21
Liggett SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2001; 2001WO-US12575
                                                                                             (LIGG/) LIGGETT S B. (SMAL/) SMALL K M.
Small KM;
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RESULT 2
AADO4761.
ID AADO
XX AADO
AC AADO
XX Huma
AC Huma
XX Huma
XX Huma
XX Huma
XX Gorc
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 21
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cyclase, ...
evels). The provided the graph of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamic acid repeat; intracerium, rock, contraction; variant; norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heat disease; CHD; chronic angina pectoris; coronary artery; coronary heat disease; CHD; chronic angina pectoris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of a human alpha-2BAR PCR primer, useful for the genotyping methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD04761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD04761 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha2B-adrenoceptor (alpha2B-AR) variant gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-611728/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCATCATCCCTTTCTCGCT 21
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ilarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                          /*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 C;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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26-APR-2001. W0200129082-A1

WO200179561-A2

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RESULT 3
AA199906
ID AA19
XX AA19
AC AA19
XX Huma
AC Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
XX Cent
XW Cent
XW Poly
XW Cent
XW WO2(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a gene encoding human alpha2B-adrenoceptor

(alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat

celement (emino acids 298-30) of 12 glutamates, in an acidic stretch of

10 la maino acids (emino acids 294-311), located in the third intracellular

11 cloop of the receptor polypeptide. The variant is obtained by deletion of

12 cloop of the glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR

13 cloop of the cated on chromosome 2. Alpha2-AR mediate many of the

14 cloop of the cated on chromosome 2. Alpha2-AR mediate many of the

15 cloop of the cated on chromosome 2. Alpha2-AR mediate many of the

16 cloop of the cated on chromosome 2. Alpha2-AR mediate many of the

17 cloop of the cated on chromosome 2. Alpha2-AR mediate many of the

18 cloop of the catedolamines, norepinephrine and

19 cloop of the catedolamines, norepinephrine and

20 cloop of the catedolamines, norepinephrine and

21 cloop of the catedolamines, norepinephrine and

22 cloop of the catedolamines, norepinephrine and

23 cloop of the catedolamines, norepinephrine and

24 cloop of the catedolamines, norepinephrine and

25 cloop of the catedolamines, norepinephrine and

26 cloop of the catedolamines, norepinephrine and

27 cloop of the catedolamines, norepinephrine and

28 cloop of the catedolamines, norepinephrine and

29 cloop of the catedolamines, norepinephrine and

20 cloop of the catedolamines, norepinephrine and

20 cloop of the catedolamines, norepinephrine

20 cloop of the catedolamines, norepinephrine

21 cloop of the catedolamines, norepinephrine

22 cloop of the catedolamines, norepinephrine

23 cloop of the catedolamines, norepinephrine

24 cloop of the catedolamines, norepinephrine

25 cloop of the catedolamines, norepinephrine

26 cloop of the catedolamines, norepinephrine

27 cloop of the catedolamines, norepinephrine

28 cloop of the catedolamines, norepinephrine

29 cloop of the catedolamines, norepinephrine

20 cloop of the catedolamines, norepinephrine

20 cloop of the catedo
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Best Local
                                                                                                                                                                                                                                                     Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                               Human alpha-2BAR third intracellular loop variant encoding
                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI99906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI99906 standard; DNA; 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary arteries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salonen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAE00989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUVA-) JUVANTIA PHARMA LTD
                                                                                                                                                                                                                     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCATCATCCCTTTCTCGCT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heinonen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kauhanen J,
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salonen
                                                                           /product= "alpha-2BAR"
/note= "sequenca"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0422985
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 A; 459 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                    "sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides of the wildtype alpha-2BAR protein (AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alhopuro P,
T, Tuomainen 7,
Valkonen V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karvonen
T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nyyssoenen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 4
AAD44388
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AC AAD4
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TI
DT 13-D
XX
DE Huma
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KW Huma
KW hype
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) postaining a sample having a polymorphic site comprising complement of; and CC (b) detecting a polymorphic site comprising nucleotide positions 901-909 CC (i), a site comprising (X) (gyggggggcg) or (B) (gyggggggtgag) at CC (positions 961-972 of (III). The method may be used for genotyping an CC positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease selected from cardiovascular CC disease, central nervous system disease selected from cardiovascular CC disease, the technique may be used to predict an individual's response CC norapinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. vohimbine, prazosin, ARC 239, CC rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl CC cyclase, MAP kinase activity, phosphorylation or inosito phosphate CC (Aligney). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide CC (Aligney).
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-2000;
10-AUG-2000;
19-OCT-2000;
Human; hypertension; alpha-2B-adrenoceptor; A hypertension; hypotensive; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIGG/)
                                                    Human alpha-2B-adrenoceptor variant DNA
                                                                                                                           AAD44388;
                                                                                                                                                          AAD44388 standard; DNA; 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 144-145; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a polymorphic
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SMALL K M.
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                               GCTCATCATCCCTTTCTCGCT 209
                                                                                                                                                                                                                                                                               GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0551744.
; 2000US-0636259.
; 2000US-0692077.
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                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site
                                                                                                                                                                                                                                                                                                                                                                                       220 A;
                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                       458
                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                Score 21; DB
Pred. No. 3.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       C; 400
                                                                                                                                                                                                                                                                                                                                                                               G;
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                                                                                                                                                                                                                                                                                                                                                                                     266 T; 0
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                   AR;
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                                                                                                                                                                                                                                                                                                                                                                                       other;
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RESULT 5
AAD0476
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XX Huma
XX Huma
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Best Local S
Matches 21
                                                                                                                                                                                                       Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectacute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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Synthetic.
                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD04762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD04762 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-2B-adrenoceptor variant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 24-26; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-2-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salonen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001FI-0000323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2002; 2002WO-FI00113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2002
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DB; AAE26633.
                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                                                                                                                            alpha2B-adrenoceptor (alpha2B-AR) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCATCATCCCTTTCTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
/*tag= a
/product=
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human alpha-2B-adrenoceptor variant
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                               1..1353
                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 C;
                          "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 24; Pred. No. 3.2; Oj. Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 G;
                             alpha2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1344;
                               (alpha2B-AR)
                                                                                                                                                                                                                                                                                    catecholamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
                                                                                                                                                                                                                               pectoris;
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0;

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RESULT 6
AA19905
AA19905
XX AA19
XX AA19
XX AA19
XX AA19
XX Huma
DE Huma
XX Huma
XX Phoi
XX Phoi
XX Geni
XX Geni
XX Hom
XX Hom
XX FH Key
FT CDS
FT CDS
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Best Local S
Matches 21
                                                                                         Homo
                                                                                                                Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR;
                                                                                                                                                                                 Human alpha-2BAR third intracellular loop encoding
                                                                                                                                                                                                                                                                  AAI99905 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element acids catids 298-309) of 12 glutamates, in an acidic stretch of 18 amino the receptor polypeptide. Alpha2B-AR gene is located intracellular loop of Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries and a disease involving as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                      18-FEB-2002
                                                                                                                                                                                                                                               AAI99905
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 27-29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scheinin M, Salumen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000; 2000WO-FI00913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JUVA-) JUVANTIA PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200129082-A1
                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                       189
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DB; AAE00990.
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                ĠĊrĊArĊArĊĊĊrrrĊrĊĠĊr 209
                                                                                                                                                                                                                                                                                                                                                        GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heinonen P, Al
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                (first entry)
     /product= "alpha-2BAR"
/note= "sequence includes a 9
                                   /*tag=
                                                           Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0422985
                                                                                                             AF009500;
                                                                                                                                                                                                                                                                                                                                                                                                                                223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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IT, Tuomainen T,
I, Valkonen V;
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                                                                                                          chromosome
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB
Pred. No. 3.2
0; Mismatches
                                                                                                           2; ds
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3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                       22;
nucleotide polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 1353;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                   DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koulu M, Pa
Nyyssoenen
                                                                                                                                                                                                                                                                                                                                                                           0,
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RESULT 7
AAD44389.
ID AAD4
XX
AC AAD4
XX
AC AAD4
XX
DT 13-D
XX
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                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site encoding an alpha-2B, CC (b) detecting a polymorphic site comprising mucleotide positions 901-909 (CC of (I)), a site comprising cytosine or guanine at position 753 of (IIV) (CC or a site comprising (A) (9990cg990cg) or (B) (9990cg9gyag) at (CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC alpha2B, alpha2A or alpha2A or alpha2, comprising detecting an CC disease, central nervous system disease selected from cardiovascular caddition, the technique may be used to predict an individual is at increased risk of developing a disease polymorphic site which correlate to disease selected from cardiovascular caddition, the technique may be used to predict an individual's response combinations of these. In CC disease, central nervous system disease and combinations of these. In CC combinations of these) or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a cyclase, Map kinase activity, phosphorylation or inositol phosphate (c evels). The present sequence is that of the third intracellular loop of cuthe human alpha-2BAR (GenBank Accession AR709500), the sequence includes alpha-2BAR variant (AA199906).
                                                                                                                                                                                                                       Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                     Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 144; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAM52117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2000; 2000US-0551744
10-AUG-2000; 2000US-0636259
19-OCT-2000; 2000US-0692077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-2001; 2001WO-US12575
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                                                                                                                                                           189
                                                                                                                                                                       1 GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                       Similarity
                                                                                                                                                    GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SB,
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SMALL K M.
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                224 A; 458
                                                                                                                                                                                                                              100.0%; Score
100.0%; Pred.
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variant (AAI99906)"
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                              C; 405
                                                                                                                                                      209
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                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                              <u>و</u>
                                                                                                                                                                                                                                                                           266 T; 0 other;
                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                              0
                                                                                                                                                                                                                                          Length 1353;
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                                                                                                                                                                                                         Gaps
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13-DEC-2002 AAD44389; AAD44389

(first entry)

standard;

DNA; 1353

ВP

Human

alpha-2B-adrenoceptor gene

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RESULT 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing
                                                                                         Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma immunopathy; AIDS; asthma; neuropathy; Alzheimer's di
                                                                                                                                                                                                                                                                                                                                                                                       The kit is also useful for selecting for clinical drug
the antihypertensive effect of compounds. The present
alpha-2B-adrenoceptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a risk of hypertension and targeting treatment in a by determining the pattern of alleles encoding a variant alpha-2-adrenoceptor -
 30-JAN-1998;
                       31-DEC-2002
                                                                                                                                      Human signalling
                                                                                                                                                                06-JUN-2003
                                                                                                                                                                                                           ACA56583 standard; cDNA; 2072
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 27-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2001; 2001FI-0000323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive; hypertension; hypotensive; gene; ds.
                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JURI-) JURILAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-667063/71
                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                   21;
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                                                                                                                                                                                                                                                                                                                                                                 1353
                                                                                                                                                                                                                                                                                            GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                BP; 223 A; 459 C; 405
98US-0016434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human alpha-2B-adrenoceptor protein"
                                                                                                                                       pathway polynucleotide
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                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35pp; English.
                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                      209
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                G.
                                                                                         adenocarcinoma; leukaemia; Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                                 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                              3.2;
                                                                                                                                       probe
                                                                                                                                                                                                                                                                                                                                          DB 24;
                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                         Length 1353;
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                                                                                                                                                                                                                                                                                                                    Indels
                                                                                         disease; microarray
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                                                                                                                                                                                                                                                                                                                                                                                                  sequence is human
                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                   Gaps
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Query Match Best Local S Matches 21

Similarity

100.0%; ilarity 100.0%; Conservative 0

0;

Mismatches

Score 21; Pred. No.

3.4; DB 25;

Length 2072; Indels

0

Gaps

0

other;

21;

Sequence

BP;

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CC The invention relates to a combination which, comprises a number of CC polynucleotide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an CC array element in a microarray for monitoring the expression of a number CC of target polynucleotides. The microarray is particularly useful in the CC diagnosis and treatment of cancer and immunopathology and neuropathology. CC The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, CC forensics and pharmacogenomics. The microarray is also useful for CC monitoring progression of diseases and for developing sophisticated CC profiles for the effects of currently available therapeutic drugs. The CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The CC array can detect changes in expression in a large number of genes coding CC for different signaling pathway populations which can be used to diagnose CC various diseases including cancer e.g. adenocarcinoma and leukaemia, CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease CC probe of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                        Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1181; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1998;
                                               at segdata.uspto.gov/sequence.html?DocID=06500938B1.
                                                                                                                       probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-352189/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCYTE GENOMICS INC
  2072
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316 A; 705 C; 660 G; 391 T; 0
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ABZ412624
ABZ4 ABZ4
XX
AC ABZ4
XX
AC ABZ4
XX
DT 04-M
DT 04-M
DT WW G pr
KW Immu
KW imm
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                                                                                                                                                                                                                                          G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Altheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; disease; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ42624 standard; DNA; 3274 BP
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                                                                                                                                                                                           gene;
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Homo

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RESULT 10
ABL32075/c
ID ABL320
XX ABL320
XX ABL320
XX Z6-MAR
XX DE Human
XX Human;
KW Human;
KW neurog
KW antiar
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                                                                                                                                                                                                                                                                                                                                                                         The present invention describes antigenic peptides (1) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC antibodies. The antigenic peptides for GPCRs are useful in detecting
CC in gene therapy. The antigenic peptides are also useful for detecting
CC antibodies. The peptides and antibodies are also useful for detecting the
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC diseases, or autoimmune diseases, growth-related diseases, cell
CC diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC diseases, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC onseess, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC close, pellepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC any other disorder in which GPCRs are involved. The antibodies may be
CC GPCR proteins given in ABP81675 to ABB82018, which are used in the
CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                 ABL32075;
                                                                                                                                                                             ABL32075
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 523pp; English
                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burmer GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-2000; 2000US-257144P
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                                                                                     immune
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DB; ABP81780.
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                 GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                            GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                      3274
                                                                                                                                                                                                                                                                                                        Conservative.
                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roush CL,
                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                         587 A; 979 C; 967 G; 741 T;
                                                                                  associated
                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                        6904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown JP;
                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                   Score 21;
Pred. No.
                                                                              gene
                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                              209
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                              SEQ
                                                                             ID
                                                                                                                                                                                                                                                                                                                  3.6;
                                                                                                                                                                                                                                                                                                                             DB 25;
                                                                             .
No
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                            0
                                                                             48.
                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                           Length 3274;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                             Gaps
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RESULT 11
AAD28365/c
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                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
30-JUN-2000; 2000DE-1032529
                    02-JUL-2001; 2001WO-EP07540.
                                                                    WO200202809-A2
                                                                                            Homo
                                                                                                                                behavioural disorder; neurological;
                                                                                                                                               Human; cytostatic;
adrenergic alpha-1
                                                                                                                                                                          Human chemically treated genomic DNA #6.
                                                                                                                      Tourette's syndrome;
                                                                                                                                                                                                                             AAD28365;
                                                                                                                                                                                                                                                 AAD28365 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6904 BP; 1326 A; 314 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fractor diagnosis and treatment cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                    1716 GCTCATCATCCCTTTCTCGCT
                                                                                                              abuse;
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                 GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 48; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                            alpha-1C-receptor;
                                                                                                             migraine; ds.
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                     (first
                                                                                                                                                     antidepressant;
                                                                                                                                                                                                                                               DNA; 6904
                                                                                                                                                                                                    entry)
                                                                                                                     smoking;
                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĀĢ
                                                                                                                                                                                                                                                                                                                                                       .0%; Score 21; DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin
                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                             sant; neuroleptic; nootropic; antiaddictive; cytosine methylation; therapy; alcoholism; gical; psychiatric; cancer; schizophrenia; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                     1696
                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ζ,
                                                                                                                                                                                                                                                                                                                                                                                         2030 G;
                                                                                                                                                                                                                                                                                                                                                                                     3233 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                 DB 24;
                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                Length 6904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, useful abnormal
                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                        Gaps
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01-SEP-2000; 2000DE-1043826.

D

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AAI9917
ID AAI99
XX AI99
XX AI99
XX AI99
XX IB-FE
XX Human
XX Human
XX POI9m
KW Centr
KW Centr
KW GenBa
XX GenBa
XX GenBa
XX IB-OC
XX IB-O
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personallty traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenia and schizophrenia, personality traits, behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2AAR; GenBank Accession AP281308; chromosome 10; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
                              17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-06920,77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 44-48; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01ek
                                                                                                                                               17-APR-2001;
                                                                                                                                                                                                                                                                   WO200179561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alpha-2AAR encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI99917 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6904 BP; 1326 A; 314 C; 2030 G; 3233 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-154759/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCATCATCCCTTTCTCGCT 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                               2001WO-US12575
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       /product= "alpha-2AAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 1350 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                გ
ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٣
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , e . i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic settencoding an alpha-2B, CC alpha2A or alpha2C or fragment or complement of; and CC of (I), a site comprising cytosine or guanine at position 901-909 CC of (I), a site comprising (A) (gyggcgggccg) or (B) (gyggcggctgag) at CC or a site comprising (A) (gyggcggccg) or (B) (gyggcggctgag) at CC or a site comprising (A) (gyggcggccg) or (B) (gyggcggctgag) at CC or a site comprising (A) (gyggcggccg) or (B) (gyggcggctgag) at CC or a site comprising (A) (gyggcgcgc) or (B) (gyggcgctgag) at CC or a site comprising (A) (gyggcgcgc) or (B) (gyggcgctgag) at CC or a site comprising (A) (gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprising (A) (gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgccg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgcgcg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgcgcg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgcgcg) or (B) (gyggcgcggcgcg) or (B) (gyggcgctgag) at CC or a site comprision (Gyggcgcgcg) or (B) (gyggcgcgcgcg) or (B) (gyggcgcgcgcg) or (B) (gyggcgcgcg) or (B) (gyggcgcgcg) or (B) (gyggcgcgcgcg) or (B) (gyggcgcgcgcg) or (B) (gyggcgcgcg) or (B) (gyggcgcgcg) or (B) (gyggcgcgcg) or (B) (gyggcgcgcgcg) or (B) (gyggcgcgcg) or (B) (gyggcgcg) or (B) (gyggcgcgg) or (B) (gyggcgcg) or (B) (gyggcgcgg) or (B) (gyggcgcgg) or (B) (gyggcgcg) or (B) (gyggcgcgg) or (B) (gyggcgcg) or (B) (gyggcg
                                                                                             predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2AAR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful determining whether an individual is at increased risk of developi disease associated with the corresponding receptor comprises detec a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 151; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIGG/) LIGGETT S B. (SMAL/) SMALL K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-611728/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SB,
                                                                 Accession AF281308).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting
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RESULT 13
AA159918
JD AA159918
AC AA19
XX AA19
XX Huma
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Best Local Similarity
Matches 20; Conserv
                                                    allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human alpha-2AAR variant encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI99918 standard;
                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation;
                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCGTCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCATCATCCCTTTCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
/*tag= a
/product= "alpha-2AAR"
replace(753,C)
/*tag= b
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         inositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 1350
                                                                                                                                                                                                                                                                                                                                                                                                               phosphate; alpha-2AAR; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
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밁 S

Sequence 1350

BP;

199 A; 490 C; 441 G;

220 T; 0 other;

92.4**%**; 95.2**%**;

Score 19.4; Pred. No. 18

DB 23;

Length 1350; Indels

٥,

Mismatches 18;

WO200179561-A2

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GXXGXGXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
ABQ47500/c
                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc alpha2A or alpha2C or fragment or complement of; and complement of comple
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular;
                                                                      Oligonucleotide
                                                                                                                                                                                      ABQ47500 standard; DNA; 1733
                                                                                                              12-JUL-2002
                                                                                                                                                      ABQ47500
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to receptor gene (I)-(III) b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 152; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (a) obtaining a sample having a polynucleotide encoding an alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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(SMAL/)
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DB; AAM52123.
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                                                             detecting cytosine methylation
                                                                                                          entry)
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by detecting a polymorphic site,
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Pred. No. 1
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CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA that contains the target C is amplified to form a labeled amplicon. CC member, of oligonucleotides and/or peptide-mucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC lasses of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method CC systems etc., particularly by detecting mutations or single nucleotide CC systems etc., particularly by detecting mutations or single nucleotide CC classes and for investigating cell differentiation. The method allows the
                             polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; 56pp + Sequence Listing; 56pp;
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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other;

밁 Ş Matches Query Match Best Local 1222 1 GCTCATCATCCCTTTCTCGCT 21 20; Similarity GCTCGTCATCCCTTTCTCGCT 1202 92.4%; ilarity 95.2%; Conservative 0, Score 19.4; Pred. No. 18; Mismatches DB 24; ۲, Length Indels 0 Gaps 0

RESULT 15 ABQ47501 ABQ47501

standard; DNA;

ABQ47501;

12-JUL-2002 (first entry)

X S X F X B X B X B X B X X X Oligonucleotide for detecting cytosine methylation SEQ ID NO

Human; Cyrosine methylation; 5'-Cpg-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.

Homo sapiens.

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                                                                                                                                                   This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (A) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory contents etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method disclosure of the invention.
                                                                      Query Match
Best Local S
Matches 20
                                                                                                                                             Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
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05-SEP-2000; 2000DE-1044543.
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                                                                      / Match
Local Similarity 95.2%; Pred. No. 18
nes 20; Conservative 0; Mismatche
512 GCTCGTCATCCCTTTCTCGCT 532
                 1 GCTCATCATCCCTTTCTCGCT 21
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Search completed: February 12, 2004, 04:01:23 Job time : 111.378 secs

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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US-09-0131-294A-1293
US-09-313-294A-1953
US-09-248-335-51
US-09-248-335-51
US-09-252-991A-16352
US-09-252-991A-16239
US-08-993-228-11
US-09-462-5618-9
US-09-511-6258-21
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Sequence 1181, Ap
Sequence 1193, Ap
Sequence 1953, Appl
Sequence 1532, A
Sequence 16352, A
Sequence 16352, A
Sequence 5, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 1, Appl
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Query Match 100.0%; Score 21; Best Local Similarity 100.0%; Pred. No.	RESULT 1 US-09-016-434-1181 US-09-016-434-1181 Sequence 1181, Application US/09016434 PATENTIANON: ASONOMARY APPLICANT: Janice Au-Young APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Seilhamer APPLICANT: COMPOSITION PATHWAY GENE EXPRESS UNMBER OF SEQUENCES: 1490 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE CALIFORNIA COUNTRY: USA ZIP: 94304 COMPUTER ENALOBLE FORM: MEDIUM TYPE: PLOPBY disk COMPUTER: BIM PC COMPATIBLE COMPUTER: BIM PC COMPATION APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH CLASSIFICATION APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH CLASSIFICATION APPLICATION DATA: APPLICATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-0002 US FELEPHANE: CALBACTERISTICS: LENGTH: 2072 base pairs TYPE: NUCLPICAL CALBACTERISTICS: LENGTH: 2072 base pairs TYPE: NUCLPICAL CALBACTERISTICS: LENGTH: 2072 base pairs TYPE: NUCLPICAL CALBACTERISTICS: LIBRARY: GENBANK L	ALIGNMENTS	C 28 15.2 72.4 36519 3 US-08-923-137 29 15.2 72.4 4403765 3 US-09-103-84 30 15.2 72.4 4411529 3 US-09-103-84 C 31 14.8 70.5 155 3 US-08-444-818 C 32 14.8 70.5 155 3 US-08-444-818 C 33 14.8 70.5 164 3 US-08-444-818 C 34 14.8 70.5 318 3 US-08-444-818 C 35 14.8 70.5 353 3 US-08-444-818 C 36 14.8 70.5 353 3 US-08-444-818 C 37 14.8 70.5 353 3 US-08-444-818 C 37 14.8 70.5 363 3 US-08-444-818 C 38 14.8 70.5 363 3 US-08-444-818 C 39 14.8 70.5 363 3 US-08-443-818 C 39 14.8 70.5 943 3 US-08-433-695 C 40 14.8 70.5 943 2 US-08-483-695 C 41 14.8 70.5 943 2 US-07-965-285 C 42 14.8 70.5 943 2 US-07-965-285 C 44 14.8 70.5 943 2 US-07-965-285 C 44 14.8 70.5 943 2 US-08-487-231 C 45 14.8 70.5 943 2 US-08-487-231
DB 4; Length 2072; 0.48;	OR THE DETECTION OF SIGNALING EXPRESSION LS, INC. Windows/MS-DOS 6.2 34		Sequence 2, Appli 10A-2 Sequence 2, Appli 00A-1 Sequence 1, Appli Sequence 3, Appli Sequence 6, Appli Sequence 5, Appli Sequence 9, Appli Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli Sequence 9, Appli Sequence 13, Appli Sequence 6, Appli Sequence 6, Appli Sequence 13, Appli Sequence 6, Appli Sequence 6, Appli Sequence 43, Appli Sequence 43, Appli Sequence 43, Appli Sequence 6, Appli

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US-09-016-434-1180
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                                                             GENERAL INFORMATION:
                                                                              Sequence 1953, Application US/09313294A Patent No. 6476212
                                                                                                                                                                                                                         Matches
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                                                 APPLICANT:
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         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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APPLICANT: Jeffrey J. Seilhamer
APPLICANT: OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                          LIBRARY: GENBANK
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                                                                                                                                                                                                                      Similarity 95.;
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                                                Lalgudi,
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (650) 855-0555
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POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
                                                Raghunath V.
                                                                                                                                                                                                                                    92.4%;
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Pred. No. 2
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US-09-252-991A-16352/c
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; TYPE: DNA
; PRANISM: Zea mays
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551803H1
US-09-313-294A-1953
                                                                                                                                                                                                                                                                                        Sequence 16352, Application US/09252991A
Patent No. 6551795
                                       SEQ ID NO 16352
LENGTH: 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word Version 7.0A SEQ ID NO 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT APPLICATION NUMBER: US/09/24,759
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER PILING DATE: 1997-September-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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SOFTWARE: PERL Progre
SEQ ID NO 1953
LENGTH: 297
                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 967
TYPE: DNA
ORGANISM: maize
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ORGANISM: Pseudomonas aeruginosa
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CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
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95.0%;
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Pred. No. 4
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Pred. No. 6
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16239
LENGTH: 1584
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16239
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US-09-252-991A-16239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: AGIIS, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 46(
TELECOMMUNICATION INFORMATION:
                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                  APPLICANT: Sandal, Thomas
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                               APPLICATION NUMBER: US/08/784,651 FILING DATE: 21-JAN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                      CITY: New York STATE: NY
                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                          ZIP: 10174
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                   4608.200-US
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Pred. No. 42;
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Pred. No. 4
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; ORGANISM: Homo sapiens
US-09-489-847-53
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US-08-993-228-11
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LENGTH: 1860
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.1%;
Best Local Similarity 94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-08-06
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al
                                                                                                                                                            tent No.
                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                  APPLICANT:
                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Genomic DNA
    TITLE OF
                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2102 base pairs
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                                                                                                                                                                                                                                                                                                                   18; Conservative
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    INVENTION:
                                                                                                                                                                                                                                                                                      GCTCATCATCCCTTTCTCGCT 21
                                                                                                                                                                         Application US/08993228
              Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
                                                                                            McCoy, John M.
LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                               Racie, Lisa A
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                                                                                                                             Kenneth
 , Michael J. SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                    77.1%;
85.7%;
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EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PZ031P1
CURRENT APPLICATION NUMBER: US/09/489,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 98 Human Secreted Proteins
                                                                                                                                                                                                                                                                 60/095,454
                 Score 16.2;
Pred. No. 82;
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Pred. No. 6
 Mismatches
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CORRESPONDENCE ADDRESS TITLE OF INVENTION:

ENCODING THEM

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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2837 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence s
                                                                                                                   LENGTH: 3430
                                                                                                                                      TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES FILE REFERENCE: Wade et al CURRENT FILING DATE: 2000-03-22 PRIOR APPLICATION NUMBER: US/09/462,561B PRIOR APPLICATION NUMBER: P07802 PRIOR APPLICATION NUMBER: P07802 PRIOR APPLICATION NUMBER: P07802 PRIOR FILING DATE: 1997-07-09 PRIOR FILING DATE: 1997-07-09 PRIOR APPLICATION NUMBER: PCT/AU98/00533 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver. 2.1
                     NAME/KEY: unsure
LOCATION: (1110)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.1%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                           ORGANISM: Equus caballus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-462-561B-9/c
                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, VURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,228
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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(1656)
                unsure
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                                                                                                                                                                                                                                                                                                                                Harrison, Bruce King, Brian W.
Reed, Kenneth C.
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87 CambridgePark Drive
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                         n at
                                                                                                                                                                                                                                                                                                                                                                Bruce T.
                     position
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Pred. No. 87;
0; Mismatches
                    1110
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Sequence 178, Application US/09634238 Patent No. 6544772 GENERAL INFORMATION:

Glenn, Matthew Havukkala, Ilkka J. Bloksberg, Leonard, N. Lubbers, Mark W. Dekker, James

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PRIOR APPLICATION NUMBER: PCT/US98/1782
PRIOR APPLICATION NUMBER: 60/070,397
PRIOR FILING DATE: 1988-08-27
PRIOR FILING DATE: 1989-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4
1 SEQ ID NO 21
LENGTH: 414
ORGANISM: Artificial Sequence
FRATURE: DANA
ORGANISM: Artificial Sequence
US-09-634-238-178/c
                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-511-625B-21/c
                                                                                                                               Query Match
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                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                    OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/511,625B
CURRENT FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Patel, Bharring.

APPLICANT: Pierce, Jacalyn H.

TITLE OF INVENTION: ATTENDATED AND DOMINANT NEGATIVEVARIANT TITLE OF INVENTION: CDNAS OF STATE: STATES AND STATEC

FILE REFERENCE: 14014,030011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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LOCATION: (2781)
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                                              340 rcagcarrecrrrereser 322
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                                                                                                  il Similarity
17; Conserv
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                                                                    3 TCATCATCCCTTTCTCGCT 21
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5. 6368828
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16; Conserv
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                                                                                                              89.5%;
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94.1%;
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                                                                                         Score 15.8; DB 4
Pred. No. 1e+02;
0; Mismatches
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Pred. No. 1.1e
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Christensson,

Anna

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RESULT 13
US-08-784-651-1/c
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LENGTH: 1322
Query Match
Beet Local Similarity 89.5
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Berka, Randy

APPLICANT: Boominathan, Karuppan

APPLICANT: Sandal, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: them and methods for using them. FILE REFERENCE: 11000.1043U1
                                                                                                                                                                                               TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Lactobacillus rhamnosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,651
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: AGT16, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sandal, Thomas
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                             MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.2%;
Local Similarity 89.5%;
les 17; Conservation
                                                                                                                                         STRANDEDNESS:
                                                                                                                                                              LENGTH: 2168 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: No. 5821102o No. 5821102disk of No. 5821102th America, Inc.
405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                           single
                                     75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                     Score 15.8;
Pred. No. 1.
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Pred. No. 1
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                                     1.3e+02;
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                                                     DB 1; Length 2168;
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                                                                            ; OTHER INFORMATION: n = a, US-09-511-625B-5
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                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: 60/056,075
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09511625B
Patent No. 6368828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserv
Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/511,625B
CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: PCT/US98/17821
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/070,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: ACYL-COA Oxidase Homologs
FILE REFERENCE: BB-1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pierce, Jacalyn H.
TITLE OF INVENTION: ATTENDATED AND DOMINANT NEGATIVEVARIANT
TITLE OF INVENTION: CDUAS OF STAT6: STAT6b AND STAT6c
FILE REFERENCE: 14014.0300ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 31
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/342,647A
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,482
EARLIER FILING DATE: 1998-07-10
                                                                                                                OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e OTHER INFORMATION: synthetic construct NAME/KEY: misc feature LOCATION: (1)...(17425)
                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                      ENGTH: 17425
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89.5%;
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  Score 15.8; D
Pred. No. 1.7e
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Pred. No. 1.
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                  .7e+02;
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                                      Length 17425;
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Page 6

Search completed: February 12, 2004, 06:07:47 Job time : 40.6829 secs B 8 3 TCATCATCCCTTTCTCGCT 21 ||| || || ||| ||| || || || 6790 TCAGCATTCCTTTCTCGCT 6772

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Run
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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15:
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1: /cgn2 6/prodata/1/pubpna/US07 PUBCOMB.seq:*
2: /cgn2-6/prodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2-6/prodata/1/pubpna/US06 NEW PUB.seq:*
4: /cgn2-6/prodata/1/pubpna/US05 PUBCOMB.seq:*
5: /cgn2-6/prodata/1/pubpna/US07 NEW PUB.seq:*
6: /cgn2-6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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     6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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                US-10-077-870-3

US-10-001-073-1

US-10-305-720-1181

US-10-325-567A-41

US-10-311-455-48

US-10-001-073-24

US-10-001-073-24

US-10-001-073-25

US-10-305-720-1180

US-10-325-567A-39
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US-09-825-923-3
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US-09-825-923-1
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Sequence 13, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1181, Appl
Sequence 48, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 46, Appl
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1.77	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	78.1	78.1	78.1	78.1	78.1		78.1	78.1		78.1	78.1	78.1	78.1		80.0	80.0	81.0	81.0	82.9
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US-10-369-493-28507	-09-844-	-09-804-291-	US-09-886-055-124	US-10-027-632-14649	-10-027-632-	-10-027-632-13485	-10-027	US-09-974-300-6869	US-10-260-238-3223	US-09-294-093B-2749	US-10-374-979-6	US-09-801-368-43	US-10-017-161-1	-10-292-	-09-804-291-4		US-09-965-422-33	-965	US-10-025-806-53	US-10-005-041A-29	-422-	-09-965	US-09-804-291-480	US-09-886-055-480	US-10-027-632-224986	US-10-027-632-224986	US-10-027-632-173743	US-10-027-632-173743	US-10-085-117-64
sequence 28507, A		12,	Sequence 124, App	Sequence 14649, A		O	134859	6869,	3223,	274	Sequence 6, Appli	43	1,	۳,	428	428,	33,	31,	53,	29,	15,	13, /	e 480,	e 480,	Sequence 224986,	Sequence 224986,		1737	Sequence 64, Appl

ALIGNMENTS

RESULT 1

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Sequence 13, Application US/10001073

Publication No. US20030113725A1

GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 21
; Sequence 1, Application US/09825923; Patent No. US20010016338A1; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
                                                                                                                                                          RESULT 2
US-09-825-923-1
                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-13
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                21; Conservative
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RESULT 4
US-10-001-073-2
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LENGTH: 1344
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NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
-09-825-923-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beat
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1 EQ ID NO 1
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                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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Salonen, Riitta
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Salonen, Jukka T
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Pred. No. 3.8;
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SEQ ID NO 3
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
TENTON: 12/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
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                                                                                                                                                                                                                                                          TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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ORGANISM: Homo sapiens
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Alhopuro, Pia
Karvonen, Matti
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Salonen, Riitta
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Salonen, Jukka T
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Pred. No. :
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Pred. No. 3.8;
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RESULT 8
US-10-305-720-1181
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; ORGANISM: Homo sapiens
US-10-001-073-1
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PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
                                                                                                 Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
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                                     APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
FILE REFERENCE: PA-0002-1 CON
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CURRENT FILING DATE: 2001-11-01
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SOFTWARE: PatentIn Ver. 2.0
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CURRENT APPLICATION NUMBER: US/10/305,720 CURRENT FILING DATE: 2002-11-26
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NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
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ORGANISM: Homo sapiens
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es 21; Conserv
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100.0%; Pred. No. 3.:
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; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
SEQ ID NO 1181
; SEQ ID NO 1181
; ELNGTH: 2072
TYPE: DNA
ORGANISM: Homo sapiens
CORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Genbank ID No. US20040010136A1 g178197
US-10-305-720-1181
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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LENGTH: 3274
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   Sequence 48, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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Publication No.
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
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CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  189 GCTCATCATCCCTTTCTCGCT
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No. US20030113798A1
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Pred. No. 3.9;
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; TYPE: DNA; Homo sapiens US-10-001-073-25
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US-10-001-073-25
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APPLICANT: Ligett, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1350
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US-10-001-073-24
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                                                                                                   Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PAtentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1350
TURNERS OF THE PROPERTY OF THE PROPER
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Best Local Similarity 95.2%;
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Best Local Similarity
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
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NAME/KEY: unsure
LOCATION: 821
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GCTCATCATCCCTTTCTCGCT 21
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                                                               Conservative
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95.2%;
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Pred. No. 23
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Pred. No. 2:
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Pred. No.
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FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 3653
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                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-39
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Best Local
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US-10-305-720-1180
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1180
LENGTH: 3604
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Best Local Similarity 95.2%;
                                                                                                                                                                                                                                                                                                                             APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1180, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roueh, Christine L.
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NAME/KEY: misc_feature
OTHER INFORMATION: Genbank ID No. US20040010136A1 g178195
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     1131
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                                                                                      Similarity
                     GCTCATCATCCCTTTCTCGCT 21
GCTCGTCATCCCTTTCTCGCT 1151
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No. US20030113798A1
                                                                    Conservative
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                                                                                  92.4%;
                                                                Score 19.4; I
Pred. No. 22;
0; Mismatches
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Pred. No. 2
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RESULT 15
US-10-311-455-46/c
; Sequence 46, Application US/10311455; Publication No. US20030143606A1
; CENERAL INFORMATION:

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APPLICANT: OLEK, Alexander
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT ETLING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 46
LENGTH: 7353
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
PRIOR INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-46
                                                                                                                       문
Search completed: February 12, 2004, 06:15:35 Job time: 124.341 secs
                                                                                                                                                                                                                              Query Match 92.4%; Score 19.4; DB 13; Length 7353; Best Local Similarity 95.2%; Pred. No. 22; Matches 20; Conservative 0; Mismatches 1; Indels 0;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Match
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Gapop 10.0 , Gapext 1.0
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em_gss_vrt:
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BQ302172
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AW916723
BH735033
                                                                               SUMMARIES
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BQ302172 QVO-BT026
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AW916723 EST348027
BH735033 BOMDM37TR
                                                  Description
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BZ627353 ih51h11.g	BZ627353		811	2	17.4	30	
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M0059C2	AZ331421		736	2	7	28	
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ej72c04	BH984874		689	Ν.	•	26	
SJNEd09	CB664045	14	665	2	•	25	
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AI978395 RZ394.R E	AI978395	9	260	2		18	
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AI113972 GH10539.5	972	9	817	4		14	
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BZ374377 ie24c01.g	Z374	29	505	٠.		10	
AJ514080 AJ514080	4080	9	458	4.	17.8	9	
BZ752631 PUDCT72TD	Z75263	29	945	7.	•	œ	
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ALIGNMENTS

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Homo sapiens (human)

ENATISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 297)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Grunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Simpson,A.J.

Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and sequence tags

URNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

ENT

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: o Column: 16 This clone was selected for full length sequencing because it
                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHC)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (31-UU-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                  contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
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20; Conserv
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IMAGE:5266354,
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7t1=QV0&t2=QV0-BT0263-
101299-072-h10&t3=1999-12-10&t4=1)
Seq primeer: put. 15 forward
Seq primeer: put. 15 forward
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High quality sequence stop: 205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="BT0263"
/note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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95.2%;
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Pred. No. 3.7e+02;
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and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW916723
AW916723.1
                                                                                                                                                                                                                                                                                                                                        Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                      Similarity
                                                                                                                                                                                                                                                                                                   This clone is available through the ATCC, tel#703-365-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               passed the following selection criteria: matched mRNA
This clone has the following problem: frame shifted.
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                                                                       /note="Vector: pBlueScript SK(-); Site 1:
Xho1; Estimated insert size approx.1 kb"
203 c 177 g 134 t
                                                                                                                             /Clone_lib="Rat gene index, normalized rat, norvegicus, Bento Soares"
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/clone="IMAGE:526354"
/tissue_type="Testis"
/clone_Tib="NIH_MGC 97"
/lab_host="DH10B"
                                                                                                                                                        /tlssue_type="mix - brain, ovailver, embryo, heart, muscle,
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                                                                                                                                                                                               /db_xref="taxon:10116"
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                                                                                                                                                                                                                                 organism="Rattus norvegicus'
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813 c 721 g 470 t
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|mol_type="mRNA"
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                    87.6%;
95.0%;
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                 Score 18.4;
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le, spleen"
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                                 619;
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Unpublished
Contact: Dean RA
Clemson University Genomics Institute
                                                                                          1 (bases 1 to 676)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
                                                                                                                                                                                     Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                                                                                                                                                                            AQ448022 676 bp DNA linear GSS 08-APR-1999 mgxb0016A14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0016A14f, genomic survey sequence.
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1 (bases 1 to 658)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
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BH735033
                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
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Fax: 301-838-0208
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSa: BOMDM37TF
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                                                                           BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/clone="BOMDM37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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95.0%;
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Pred. No. 1.4e+03;
0; Mismatches 1
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oleracea genomic clone BOMDM37,
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TITLE
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Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                         DNA is from a doubled haploid Seq primer: TR
                                                                                                                                                9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                              Other_GSSs: BOGVT08TF
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu; eurosids II; Brassicales; Brassicaceae; Brassica
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Fax: 864 656 4293
                                                                                                                                                                                                                                Contact: Chris
                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH573939.1 GI:17825778
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/clone lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."

15 a 204 c 150 g 206 t lothers
                                                                             sheared ends
                                                                                                                                   cdtown@tigr.org
                                       1. .839
                                                       Location/Qualifiers
organism="Brassica oleracea"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
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95.0%;
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Best Local :
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BZ752631 945 bp DNA linear GSS 10-MAR-2003 PUDCT72TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa157L24, genomic survey sequence.
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PUDCT72TB ZM 0.6 1.0 KB Z
genomic survey sequence.
B2752626
B2752626.1 GI:28904975
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Similarity 95.0%;
Similarity 95.0%;
                                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA Tal: 301-838-5843 Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clade; Panicoideae; Andropogoneae;

(bases 1 to 909)

Whitelaw, C.A., Quackenbush, J., Van
, A., Fraser, C.M., Yuan, Y., San Migu
Maize Genomics Consortium
Unpublished
                                                                                                          CTCATCATCCCTTTCACGCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: PUDCT72TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                    /db xref="laxon:4577"
/db xref="laxon:4577"
/clone="ZMMBTa157L24"
/clone="Ibb="ZM_0.6_1.0_KB"
/clone="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
ZOT selected genomic DNA library"
178 c 169 g 282 t
                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/db xref="taxon:3712"
/clone="BOGVT08"
/clone lib="BOGV"
/clone lib="BOGV"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 106 c 200 g 259 t
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Pred. No. 1.6e.
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Pred. No. 1.
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ZMMBTa157L24,
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AJ514080/c
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ORIGIN
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AUTHORS
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ORGANISM
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KEYWORDS
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Best Local
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 CTCATCATCCCTTTCACGCT 546
                                                                                                                                                                                     Gossypium hirsutum (upland cotton)
Gossypium hirsutum
Gossypium hirsutum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; rosids
; eurosids II, Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 458)
Suo,J., Liang,X. and Xue,Y.
The construction of a cDNA library from the ovule of Gossypium
hirsutum and its EST analysis
                                                                                       Centre of Developmental Biology
The Institute of Genetics and Developmental Biology CAS
Nanyitiao 3, Zhongguancun, Haidian, Beijing, 100080, Chi
Location/Qualifiers
                                                                                                                                                                      Contact: Suo J
                                                                                                                                                                                                                                                                                                                                                                                                 AJ514080
AJ514080 Gossypium hirsutum ovule first day the flower opens Gossypium hirsutum cDNA clone suo86d07r3, mRNA sequence.
AJ514080
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EST.
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Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-5843
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 945)
1 (clases 1 to 945)
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GSS.
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="zwMBTa157L24"
/clone="ZwMBTa157L24"
/clone="tector: pCR4-TOPO; Site_1: Ec
COT selected genomic DNA library"
a 183 c 174 g 293 t
/db_xref="taxon:3635"
/clone="suo86d07r3"
                         /organism="Gossypium hirsutum
mol_type="mRNA"
/cultivar="Zhongmian12"
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95.0%;
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Pred. No. 1
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JOURNAL COMMENT
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE374377 505 bp DNA linear GS 1e24cO1.g2 WGS-ZmaysF (DH5a methyl filtered) Zea mays 1e24cO1 5', genomic survey sequence.
BZ374377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PO Box 100, Cold 9
Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 505)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: ie24 row: c colu
Seq primer: -21M13UnivRev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mccombie@cshl.org
Column: 01
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                                                                                    Similarity
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GCTCATCATCCCTCTCTCT 458
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                                                                                                                                                    /clone lib="WGS-ZmaysF" (DH5a methyl filtered) "
/clone lib="WGS-ZmaysF" (DH5a methyl filtered) "
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."
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                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                     /lab_host="DH5a"
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/clone="ie24c01"
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90.5%;
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90.5%;
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                                                                 Score 17.8; D
Pred. No. 2.2e
0; Mismatches
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No. 2.1e+03;
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ACCESSION
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BU100970/c
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                                                                                   BE427478/c
                                                                                                            RESULT
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Best Local S
Matches 19
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                                                                                                                                                                               397
PSR7068 ITEC PSR Wheat Pericarp/Testa Library Triticum aestivum cDNA clone PSR7068, mRNA sequence.
BE427478
                                                                BE427478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence
quality sequence with phred score less than 20
Seq primer: SK primer.
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Anderson,O.D., Chao,S., Chin,A., Close,T.J., Crossman,C., Gusta,J.P., Lazo,G.R., Pham,J., Rausch,C.J., Ross,K., Wilson,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                      /note="vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown for four
days under hydroponic conditions with 1ppm aluminum, root
tips were excised and snap frozen, and total RNA was
prepared at University of Missouri in the JP Gustafson lab
(Ross). Poly(A) RNA was purified, a cDNA library was made,
and the cDNA clones were in vivo excised to give
pBluescript SK(-) phagemids in the TJ Close lab (Chin) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="WHE3360_A09_A18"
/tlssue_type="Root tip at 1.0 to 1.5
/tlssue_type="RootIng"
/dev_stage="SeedIng"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Chinese Spring"
/db_xref="taxon:4565"
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/mol_type="mRNA"
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Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service,
West Area, Western Regional Research Center
West Area, Mestern Albany, CA 94710, USA
                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 718)
Anderson,O.D., Chao,S., Chin,A., Close,T.J., Crossman,C., Gustafson,J.P., Lazo,G.R., Pham,J., Rausch,C.J., Ross,K., Wilson,C. and Woo
                                                                                                                      Genomes - C
Unpublished
                                                                                                                                                              The structure and
                                                                                                                                                                                                                                                                                                                                  Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHE3361_A09_B17ZS Chinese library Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                          BU101040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: paul.bailey@bbsrc.ac.uk
International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Bailey P
Cereals Group, John Innes Centre
Norfolk, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
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                                                                                                                                     Chinese Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="pericarp/testa"
/dev_stage="3:1 mix 10:20 days post anthesis"
/clone lib="ITEC PSR Wheat Pericarp/Testa Library"
/note="Vector: Lambda ZAP II (Stratagene)"
122 c 160 g 162 t 16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
/clone="PSR7068"
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/mol_type="mRNA"
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90.5%;
                                                                                                                               function of the expressed portion Spring aluminum-stressed root tip
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Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 718 bp mRNA linear EST 29-AUG-2002
s Spring aluminum-stressed root tip cDNA
n cDNA clone WHE3361_A09_B17, mRNA
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AI113972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 GCTCATCATCCCTTTTCCGCT
Fax: 510 486 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003459: arm:2R [17805870,18105620] estimated-cyto:5982-5902: 04/10/2001 Plate: GH.105 row: D column: 3

High quality sequence stop: 579
                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                         Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
                                                                                                                                                                                                 On Sep 2, 1998 this sequence version replaced Other_ESTs: GH10539.3prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AII13972 817 bp mRNA linear EST 23-APR-2006H10539.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH10539 5 similar to CG12781: FBan0012781 located on: 2R 59B4-59B4;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                    Contact: Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI113972.2
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Fax: 5105595818
Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence with phred 
Seq primer: SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: ECORI; Site 2: XhoI; Plants were grown for four days under hydroponIc conditions with lypm aluminum, root tips were excised and snap frozen, and total RNA was prepared at University of Missouri in the JP Gustafson lab (Ross). Poly(A) RNA was purified, a cDNA library was made, and the cDNA clones were in vivo excised to give palluescript SK(-) phagemids in the TJ Close lab (Chin) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Seedling"
/lab_host="E. coli SOLR"
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/tissue_type="Root tip at 1.0 to 1.5 mm stage"
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Pred. No. 2.
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                                                                                                                           94720,
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                                                                                                                                                                                                                   gi:3514775
                                                                                                                                                                                                                                                                                                                                                           Muscomorpha;
                                                                                                                                                                                                                                                                                             Su, C., Tsang, G.,
                                                                                                                                                                                                                                                                                                                                                                     Pterygota;
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RESULT 15
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  Query Match 84.0
Best Local Similarity 90.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.8%; Score 17.8; DB 9; Length 817; Best Local Similarity 90.5%; Pred. No. 2.7e+03;
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ESM Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.

El (bases 1 to 971)

Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,

Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,

Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,

Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,

Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae

Onter, Marchael Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae
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HWM003.Dl1 ITEC HWM Barley Leaf Library Hordeum vulgare subsp.
vulgare cDNA clone HWM003.Dl1, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                          Email: herrman@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
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pOT2. Plasmid cDNA library."
a 213 c 219 g 229 t
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Search completed: February 12, 2004, 06:05:45 Job time: 1147.79 secs

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Pred. No. 8 the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 17.8 17.8 17.8 17.8 17.8 17.8 17.8 17.4 17.4 Query Match 68883 91966 104435 107529 107529 110865 114800 125856 154961 157808 174999 174099 174099 174099 22842 81920 153648 181905 213688 259219 259219 2593336 183336 218434 201844 275605 Length B 29212292129972292 ABO01925 CNS05TCL AB013182 AC128772 AC128772 AC101808 CNS01AX1 AB020667 AC101818 AC107911 AC118708 AC107911 AC118708 AC123567 AC1235684 AC123567 AC1235694 AC026655 AC121310 AX548756 AF005900 AC092603 AC019708 AC008211 AE003755 AC106994 AC097749 HSA325747 AX350490 AF316895 AX350489 AX350489 AR270618 HUMADRA2RA IJ AC092603 Homo sapi AC019708 Drosophil AC018210 Drosophil AC008211 Drosophil AC008211 Drosophil AE003755 Drosophil AE003755 Drosophil AE0013925 Deinococc AL355102 Human chr AE013182 Thermoana AC123100 Rattus no AC123100 Rattus no AC1231072 Rattus no AC1231072 Rattus no AC1231073 Rattus no AC123101 Botrytis AE0101893 Mus muscu AC101998 Mus muscu AC1016292 Homo sapi AC016292 Homo sapi AC016292 Homo sapi AC016305 Homo sapi AC012310 Human DNA AP005840 Oryza sat AC021340 Homo sapi AC123130 Homo sapi AC123130 Homo sapi AC123131 Homo sapi AC121108 Mus muscu AC111108 Mus muscu AC111108 Mus muscu M38742 Human alpha AJ325747 Homo sapi AX350490 Sequence AF316895 Homo sapi AX350489 Sequence AR270618 Sequence AR270618 Sequence M34041 Human alpha AX548756 Sequence AF005900 Homo sapi AX350502 Sequence S67316 alpha 2-adr Description AC094595 Rattus

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TITLE JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	rocus	AX350502	RESULT 1
Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 14 25-OCT-2001;	Liggett, S.B. and Small, K.M.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX350502.1 GI:18616098	AX350502	Sequence 14 from Patent WO0179561.	AX350502 21 bp DNA linear PAT 06-FEB-2002		

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RESULT 3
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Location/Qualifiers
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Identification in islets of Langerhans
2-adrenergic receptor
Diabetes 43 (1), 127-136 (1994)
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IAKKSNRRGPRAKGGPGGGESKQPREDHGGALASVASAREWGHSKSGE
KEEGETPEDTGTRALPASWAALPNSGQGQKEGVCGGSPEDEAEEEEEEEEECEPQAVP
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Institute of Neuroscience 155, Sect II, Li-Noon St.
Taipei, Taiwan, 11221 ROC.
Location/Qualifiers
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                                               Homo sapiens NB1-818S.
AJ325747
AJ325747.1 G
Homo sapiens
              Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; H
1 (bases 1 to 885)
Chang, A.C., Ho, T.F. and Chang, N.C.
In vitro amplification by polymerase chain
gene encoding the third subtype of alpha-2
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M38742
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LIAKRSNRRGPRAKGBPGQGESKQPRPDHGGALASAKLASVASAREVNGHSKSTG
EKEEGETPEDTGTRALPESWAALPNSGQGQKEGVCGASPEDBAEEEEEEEEEEEEEE
QAVPVSPASACSPPLQOPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFT
FVLAVVIGVFVLCWFPFFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="alpha-2-adrenergic receptor"
/protein id="AAA62823.1"
/db_xref="GDB:G00-120-540"
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/cell_type="neuroblastoma"
/tissue_type="neural"
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mol_type="genomic DNA"
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Eukaryota;

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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2 (bases 1 to 1030)
2 Rabarovsky, E.R.
Direct Submission
Submitted (16-MAY-2001) Microbiology
Submitted (16-MAY-1001) Microbiology
                                                                                                                                               21;
             Homo sapiens alpha
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(bases 1 to 1030)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R. NotI flanking sequences: a tool for gene discovery and verification of the human genome
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="NB1-8185"
a 329 c 308 g 182
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1 (bases 1 to 1344)

Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.

Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization biological control of the series of the kinase-mediated phosphorylation and desensitization biological control of the series of the kinase-mediated phosphorylation and desensitization biological control of the series of the seri
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LPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLA
TLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGA
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APQNLFLVSLAAADILVATLIIPFSLAANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
LCAISLDRYMAVSRALEXVASKATPRRIKCIILTVWLIAAVLSLPPLIYKGDQGPOPRG
RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
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/product="alpha 2B adrenergic receptor"
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/db_xref="GI:12698670"
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/mol_type="genomic DNA"
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Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-2 adrenergic receptor polymorphisms patent: WO 0179561-A 1 25-CCT-2001; Liggett, Stephen B. (US); Small, Kersten Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2072)

Lomasney,J.W., Lorenz,W., Allen,L.F., King,K., Regan,J.W., Yang-Feng,T.L., Caron,M.G. and Lefkowitz,R.J.

Expansion of the alpha 2-adrenergic receptor family: cloning characterization of a human alpha 2-adrenergic receptor subty the gene for which is located on chromosome 2

Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                                           alpha-2-adrenergic receptor; receptor-coupled G protein.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human alpha-2-adrenergic receptor (alpha-2 c2) gene,
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/mol_type="genomic DNA"
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                                         22842 bp
Homo sapiens BAC clone RP11-139J6
AC092603 AC073396
AC092603.2 GI:16303510
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Cayla,C., Schaak,S., Bouloumi
Alpha2C2-adrenergic receptor
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Homo sapiens alpha2B-adrenergic
complete cds
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Cayla, C., Schaak, S.,
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LPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
VLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYS
                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MDHQDPYSVQATAAIAAAITFIIIPTIFGNALVILAVCTSSISH
APQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVVLALDVLFCTSSIVH
LCALSLDRYMAVSRALEYNSKRTPRRIKCIILTVWLLAAVISLPPLIYKGDQGFQPRG
RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
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/product="alpha2B-adrenergic receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_id="AAB62558.1"
db_xref="GI:2245628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="alpha2C2AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="adrenergic receptor"
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                                                                             sequence
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                                                                                                                                                     Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Oct 20, 2001 this sequence version replaced gi:14916188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO 63108, USA
4 (bases 1 to 22842)
Waterston, R.H.
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Submitted (23-OCT-2001) Genome
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Submitted (20-OCT-2001) Genome
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The sequence of Homo sapiens BAC clone RP11-139J6
Unpublished (2001)
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Sulston, J.E. and Waterston, R.
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Center: Washington University Genome Sequencing Center Center code: WUCSC
Web site: http://genome.wustl.edu/gsc
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Freng Tateno, M., Catanase, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org Frengen, E., one male from Jong

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FEATURES
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The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574O17, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574O17.
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db_xref="taxon:9606"
chromosome="2"
                              note="match to EST BF475329 (NID:g11546156)"
                                                                                                  note="match to EST
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note="similar to Homo sapiens EST T39448 (NID:g647179)
                                                                                                                                                                note="match to EST AI733093 (NID:g5054206) oj40h05.x5"
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                                                                note="match to EST BF475329
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                                                              (NID:g11546156)"
                                                                                               (NID:g5339305) oj40h05.y5"
                                                                                                                             (NID:g3002438) oj40h05.s1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 21; I Similarity 100.0%; Pred. No. 9. 21; Conservative 0; Mismatches
              Rockville, MD, USA
This sequence was identified as CDM:10210696 by the submitter.
For more information on this record e-mail to fly@celera.com.
FOR MOTE: This is a 'working draft' sequence.
* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
                                                                                                                                                                               HTG; HTGS_PHASE2.

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Behydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster, ***
AC019708
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAAGCCCCACCATGGTCGGGT 21
                                                                                                                      Direct Submission Submitted (30-DEC-1999) Celera Genomics,
                                                                                                                                                                                                                                                                                              AC019708.1
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                                                                                                                                                                         (bases
                                                                                                                                                      and Venter, J.C.
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14060. .14247
/notee="similar to Homo sapiens EST AL549866
(NID:g12886265)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match to EST AA836522 (NID:g2910841) od22d08.s1"
7173 c 6248 g 4624 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="CDG_island (%GC=74.2, o/e=0.90, #CDGs=191)"
14900. .15218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="similar to
(NID:g8082456)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to Homo sapiens EST AL544609
(NID:91877089)"
E004 18407
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(NID:g12933576)"
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                                                                                                                                                                         1 to 81920)
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                                                                                                                                                                                                                                                                                              GI:6665189
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9.9;
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JOURNAL REFERENCE
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2 (bases 1 to 153648)

3 (bases 2, C., Chew,M., Ciesiolka,L.,

Butenhoff,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,

Doyle,C.M., Farfan,D.E., Galle,R., Karra,K., Kearney,L.,

Hoskins,R.A., Houston,K.A., Lummasti,S.R., Karra,K., Kearney,L.,

Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,

Moshrefl,A.R., Moshrefl,M., Nixon,K., Pacleb,J.M., Park,S.,

Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,

Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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19; Conser
                                                                                                                              shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                             Submitted (29-JUL-1999) Drosophila Genome Center, Lawrenc Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 27, 2001 this sequence version replaced gi:6633919
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1 (Dases 1 to 153648)
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster, chromosome BACR08G22, complete sequence.
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                                                                                                                                                                                                                                           Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                             Sequence submitted by:
Berkeley Drosophila Genome Project
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                                                                                                                                                                                                            This sequence was assembled using end sequences from a whole genome
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                                                                      d relationship to other sequences, please visit our sequenc chive Web site (http://www.fruitfly.org/sequence/) or send bdgp@fruitfly.berkeley.edu.
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16012 c 16326 g 2
/organism="Drosophila melanogaster"
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Pred. No. 3.3e+02;
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Friee,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattel,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M., and Venter,J.C.
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                                                                                                                        Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                  Laboratory, MS 64-121, Berkeley, CA 94
                                                                                                                                                                                                                                              Submitted (29-JUL-1999) Drosophila Genome Center, Laboratory, MS 64-121, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park, Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zaveri, J.S., Smith, H.O., Rubin, G.M. Sequencing of Drosophila chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOLL,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center, A., Champe, M., Davenport, B.B., Dietz,S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 181905)
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                     Sequence submitted by:
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Result No.	Score	Query Match	Query ore Match Length DB II	BB	ID	
	21	100.0	21	23	AAI99908	Human alpha-2BAR g
ი 2	21	100.0	65	24	ABN32100	Rat spliced transc
c 3	21	100.0	1344	22	AAD04761	Human alpha2B-adre
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ი თ	21	100.0	1344	24	AAD44388	Human alpha-2B-adr
ი ი	21	100.0	1353	22	AAD04762	Human alpha2B-adre
c 7	21	100.0	1353	23	AAI99905	Human alpha-2BAR t
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222		24 20 25	22 25 22	19	222222	1 2 2 5 5 9 5 5 5	125 25 23 23 23
ABQ87681 ABA90193 ABX33717	AAH46862 AAS36182 AAS36183	AAD41400 AAT58505 AAV84039 ABQ81032	AAL28410 AAI85859 AAQ71655 AAS28640 AAH46866 ABX72202	AAV50431 AAS59566	AAK53308 AAK53308 AAI61088 AAK52324 AAK52323	ABX70470 AAD47687 ABA17086 ABZ19949 AAV50488	AAQ14151 AAT59499 ACA56583 ABZ42624 AAS92399 ABV07991 ABA12198 AAI98095
Human oestrogen re Human oestrogen re Gene encoding huma	an 25278 sulf an cardiovasc an cardiovasc	NZMS- CDNA e ncodin ndothe	Human SNP oligonuc Human polynucleoti Sequence encoding Genomic sequence # Human 25278 sulfat Human NOVX polynuc	Streptomyces clavu Propionibacterium	Human polynucleoti	DNA encoding human Human kinase prote Human nervous syst Group III cDNA can Streptomyces clavu	Human alpha 2 beta Human alpha-2b adr Human signalling p Human alpha 2b-adr DNA encoding novel Human prostate exp Human neurous syst

ALIGNMENTS

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RESULT 1
AA19908
ID AA19908
XX AA19
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XX Huma
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PF 17-1
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10-AUG-2000; 2000US-0636259
19-OCT-2000; 2000US-0692077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-2BAR genotyping PCR primer SEQ ID NO
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Liggett SB,
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                                                                                            (LIGG/) LIGGETT S B. (SMAL/) SMALL K M.
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Genotyping an alpha-2B, determining whether an

, 2A, or 2C adrenergic receptor gene useful for individual is at increased risk of developing a the corresponding receptor comprises detecting

WPI; 2001-611728/70

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Best Local S
Matches 21
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32100/с
                                                                                                                                Human; splice
                                       28-JUL-2000; 2000US-221607P
02-MAY-2001; 2001US-287724P
        Shoshan
                                                               20-JUL-2001; 2001WO-IB01903
                                                                                07-FEB-2002.
                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (a) obtaining a sample having a polynucleotide encoding
alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease associated with the a polymorphic site -
                                                                                                WO200210449-A2
                                                                                                                                                        Rat spliced
                                                                                                                                                                         15-JUL-2002
                                                                                                                                                                                          ABN32100
                                                                                                                                                                                                         ABN32100 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor gene (a) obtaining
                        (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obtaining a sample waveley a project of; and hazk or alpha2C or fragment or complement of; and detecting a polymorphic site comprising nucleotide positions 901-909 detecting a polymorphic site comprising nucleotide position 753 of (IIV)
                                                                                                                                                                                                                                                                                 21;
                                                                                                                                mouse; rat; splice transcript; detection; RNA transcript;
variant; transcriptome; oligonucleotide library; ss.
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                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                AAAGCCCCACCATGGTCGGGT
                                                                                                                                                                                                                                                 AAAGCCCCACCATGGTCGGGT
                                                                                                                                                                                                                                                                                                                 BP;
       Wasserman
                                                                                                                                                        transcript detection oligonucleotide SEQ ID NO:4848
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112; 163pp; English
                                                                                                                                                                                                                                                                                                                                genotyping
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                                                                                                                                                                                                                                                                                                                A; 7 C; 6 G;
                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genotyping an alpha-2B, 2A,
by detecting a polymorphic s
                                                                                                                                                                                                                                                                                                                                 methods of the invention.
        Mintz
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                                                                                                                                                                                                                                                                                        Score
Pred.
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                                                                                                                                                                                                                                                                                                                3 T; 0 other;
       'n
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                       21; DB 23
. No. 0.86;
       Mintz
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                                                                                                                                                                                                                                                                                               23;
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       Faigler S;
                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, or 2C adrenergic site, comprising;
                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , comprising;
an alpha-2B,
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                Gaps
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detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hobelding.
                                                                                                                                                                                                                                                                                                                                                                                                               the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    several oligonucleotides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID 4848; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental-specific genes
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                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting
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Best Local S
Matches 21
 45
                                 21;
                                         Similarity
AAAGCCCCACCATGGTCGGGT
           AAAGCCCCACCATGGTCGGGT
                                larity 100.0%;
Conservative
                                       100.0%; Score 21; DB 2
100.0%; Pred. No. 0.93;
                                0,
               21
25
                                 Mismatches
                                                24;
                                0;
                                               Length
                                 Indels
                                                 65;
                                0
                                Gaps
                                0
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Sequence 65

BP; 13

Α;

22 C; 21

<u>ი</u>

9 T; 0

other;

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RESULT 3
AAD04761/c
ID AAD0477
XX AAD0477
AC AAD047
AC AAD047
XX O4-JUL
XX O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha2B-adrenoceptor (alpha2B-AR) variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUL-2001
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Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.

sapiens.

/*tag= a /product= "Human alpha2B-adrenoceptor (alpha2B-AR) variant protein" Location/Qualifiers

WO200129082-A1

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RESULT 4
AAI99906/c
ID AAI99906;
XX
AC AAI99906;
XX
DT 18-FEB-2002 (first of the control of the 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 294-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snapir A,
Scheinin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                                                                                                                                                                                                                                                                                    Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human alpha-2BAR third intracellular loop variant encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1344 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA molecule encoding variant specific adrenoceptor protein with leletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy.
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, Salonen JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kauhanen
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                                                /*tag= a "Apha-2BAR" /product= "alpha-2BAR" /note= "sequence is deleted for a 9 nucleotides ! polymorphic site found at nucleotides ! of the wildtype alpha-2BAR protein (AA)
                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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T, Tuomainen T,
, Valkonen V;
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Pred.
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T, Lakka
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Nyyssoenen
                                                        protein (AAI99905)
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len K;
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                                                                                      901-909
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RESULT 5
AAD44388/c
ID AAD443
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AC AAD443
XX
DT 13-DEC
XX
DB Human
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XW Human;
XW Human;
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                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                           CC (b) detecting a polymorphic site comprising unclectide positions 901-909 (C) of (I), a site comprising cytosine or guanine at position 753 of (IIV) (C) or a site comprising (A) (gggggggcg) or (B) (gggggggggg) at (C) or a site comprising (A) (ggggggggcg) or (B) (gggggggggg) at (C) or a site comprising (A) (ggggggggcg) or (B) (gggggggggg) at (C) or site on 961-972 of (III). The method may be used for genotyping an (C) or site of the polymorphic site which correlate to disease selected from cardiovascular (C) or site of the correlate to disease selected from cardiovascular (C) or site of the system disease and combinations of these. In (C) or site of the system disease and combinations of these or antagonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and (C) or site of these or antagonist (e.g. yohimbine, prazosin, ARC 239, (C) or sumplicate of the polymorphic site and correlated to activity or cyclase, MAP kinase activity, phosphorylation or inositol phosphate (C) (cyclase, MAP kinase activity, phosphorylation or inositol phosphate (C) (polymorphic site found at nucleotides 901-909 of the wildtype gene (C) (AA199905).
                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                             AAD44388 standard; DNA; 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to genotyping an alpha-2B, 2A, or receptor gene (I)-(III) by detecting a polymorphic site, (a) obtaining a sample having a polymucleotide encoding alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 144-145; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genotyping an alpha-2B, 2A, or 2C adrenergic receptor determining whether an individual is at increased risk
                                                                                                  AAD44388;
                                                                                                                                                                                                                                                                                                                    Sequence 1344
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                                                                                                                                                                                                                        AAAGCCCCACCATGGTCGGGT
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; 2000US-0636259.
; 2000US-0692077.
                                                                                                                                                                                                                                                           100.0%;
ilarity 100.0%;
Conservative (
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Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                      266
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                                                                                                                                                                                                                                                                                                                        other;
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                                                                                                                                                                                                                                                                                         Length 1344;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2C adrenergic, comprising;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aп
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-2B,
                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                              Gaps
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Human; hypertension; alpha-2B-adrenoceptor; hypertension; hypotensive; variant; gene; di

hypotensive; variant; gene; ds

AR;

antihypertensive;

0

Human alpha-2B-adrenoceptor variant DNA

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THE PROOF OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
AAD04762/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local S
Matches 21
                                                                                                                                                          Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine norepinephrine; epinephrine; therapy; vascular contraction; coronary attery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                 Cbs
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                               Human alpha2B-adrenoceptor (alpha2B-AR) gene.
                                                                                                                                                                                                                                                                                                                                                                                 04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD04762 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-2B-adrenoceptor variant DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a risk of hypertension and targeting by determining the pattern of alleles encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salonen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2002
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 AAAGCCCCACCATGGTCGGGT 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-667063/71.
)B; AAE26633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
/*tag= a
/product=
protein"
                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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/product= "Human alpha-2B-adrenoceptor variant
protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1353
"Human alpha2B-adrenoceptor (alpha2B-AR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment
a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1344;
                                                                                                                                                                                                                                   catecholamine;
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RESULT 7
AA199905/c
ID AA19999
XX AA19999
XX IA-FEB
XX I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino cc data (amino acids 294-311), located in the third intracellular loop of CC alpha2-AR mediate many of the physiological effects of the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. CC alpha2B-adrenoceptor is useful for treating a manmal suffering from CC vascular contraction of coronary arteries and a disease involving CC as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as prinzmetal's variant form or acute myocardial confercion (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 21
                                                                                                                                                                             Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2BAR; GenBank Accession AF009500; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                   Human alpha-2BAR third intracellular loop encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI99905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI99905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 27-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scheinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JUVA-) JUVANTIA PHARMA LTD OY
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                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 AAAGCCCCACCATGGTCGGGT 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAGCCCCACCATGGTCGGGT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
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M, Salonen JT,
, Kauhanen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; ilarity 100.0%; Pred. No. 1 Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
/*tag= a
/product= "alpha-2BAR"
/note= "sequence includes
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-F100913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 A; 459 C; 405 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37pp;
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T, Tuomainen T,
Valkonen V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karvonen
T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Nyyssoenen
                                                                                                                                                                                                                             kinase activity
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a 9

nucleotide polymorphic

site

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RESULT 8
AAD44389/c
ID AAD443
XX
AC AAD443
XX
AC AAD443
XX
DT 13-DEC
XX
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                                                                                                                                                                                                                                                                                                                                          CC of (I), a site comprising cytosine or guaning method for the comprising (A) (9990c9990cc9) or (B) (9999ct993) at CC positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2 comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, BHT93 and CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, bentolamine and combinations of these) by detecting the polymorphic site and correlated to adenylyl CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR (GenBank Accession AF009500), the sequence includes a pucleotide polymorphic site at nucleotides 901-909, absent in the CC alpha-2BAR variant (AAI99906).
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I) (III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorbide encoding an alpha-2B, alpha2A or ralpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease associated with the a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                     13-DEC-2002
                                                                                           AAD44389
                                                                                                                                                                                                                                                                                                                                      Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 144; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611728/70.
P-PSDB; AAM52117.
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10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                        AAD44389;
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SMALL K M.
                                                                                                                                                                                                            AAAGCCCCACCATGGTCGGGT 21
                                                                                           standard;
                                                                                                                                                                                      AAAGCCCCACCATGGTCGGGT 666
                                                                                                                                                                                                                                                                Conservative
                   (first
                                                                                           DNA;
                   entry)
                                                                                                                                                                                                                                                                                100.0%;
                                                                                             1353
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                                                                                                                                                                                                                                                            0;
                                                                                             ВP
                                                                                                                                                                                                                                                                              Score 21; DB 23; Length 1353; Pred. No. 1.1;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                            Gaps
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RESULT 9
AAQ14151/c
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                                                                                                                                                                                                                                                                                á
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
                                                                                                                                                          06-JAN-1992
                                                                                                                                                                                                     AAQ14151 standard; DNA; 2064 BP
                                                                                                                                                                                                                                                                                                                                                   Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing
                                                                                        Homo
                                                                                                             Neurotransmission;
                                                                                                                                  Human alpha
                                                                                                                                                                               AAQ14151;
                                                                                                                                                                                                                                                                                                                                                                          alpha-2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 27-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human alpha-2B-adrenoceptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2001; 2001FI-0000323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JURI-) JURILAB LTD OY
                                                                                                                                                                                                                                                                                                                                                                                   antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                        sapiens
                                                                                                                                                                                                                                                            989
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                                                                                                                                                                                                                                                                                  \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
                                                                                                                                                                                                                                                            AAAGCCCCACCATGGTCGGGT
                                                                                                                                                                                                                                                                         AAAGCCCCACCATGGTCGGGT 21
                                                                                                                                  N
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                        (first entry)
                                                                                                                                  beta
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                                         Location/Qualifiers
288..1752
/*tag= a
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1..1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "Human alpha-2B-adrenoceptor protein"
                                                                                                            adrenaline;
                                                                                                                                  adrenergic receptor gene.
                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                          gene.
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                                                                                                                                                                                                                                                                                                                    Score 21;
Pred. No.
                                                                                                                                                                                                                                                            666
                                                                                                            epinephrine; NGC-alpha2beta;
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01-OCT-1991

US5053337-A

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Best Local S
Matches 21
Assay for alpha-2b adrenergic receptor ligands - using
                       P-PSDB; AAW11804.
                               WPI; 1997-107576/10
                                                Hartig
                                                                                          30-OCT-1989;
30-MAY-1991;
                                                                  (SYNA-)
                                                                                   22-OCT-1992;
                                                                                                                     22-OCT-1992;
                                                                                                                                     21-JAN-1997.
                                                                                                                                                      US5595880-A.
                                                                                                                                                                                                                        Alpha-2b adrenergic epinephrine; signal
                                                                                                                                                                                                                                                   Human alpha-2b
                                                                                                                                                                                                                                                                    25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                                              AAT59499
                                                                                                                                                                                                                                                                                                             AAT59499 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone NGC-alpha2beta was isolated from a human spleen genomic library by screening with a fragment of the human 5-HTIA receptor gene. The gene can be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2064 BP; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated DNA encoding human adrenergic receptor - for detecting nucleic acids encoding alpha, 2-beta adrenergic receptor, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-310087/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEUROGENETIC CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                     1084 AAAGCCCCACCATGGTCGGGT 1064
                                                 PR,
                                                                SYNAPTIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Fig 2; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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(first en
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                                                                               89US-0428856.
91US-0707604.
92US-0965040.
                                                                                                                  92US-0965040
                                                                                                                                                                                                                                             adrenergic receptor genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hartig
                                                                                                                                                                              Location/Qualifiers
288..1751
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                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                     receptor; adrenoceptor; adrenaline; transduction; neurotransmitter; lig
                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                            В₽
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       390 T; 0
                                                                                                                                                                                                                                              DNA clone.
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membranes

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RESULT 11
ACAS6583/G
AID ACAS65
XX ACAS65
XX O6-JUN
XX Human;
XW Human;
XW Human;
XW Human;
XW IMMUNO
OS Homo s
XX US6500
XX INCY-
PF 30-JAN
XX ACAS65
PF 30-JAN
XX WPI; 2
XX ACAS65
PF 30-JAN
XX INCY-
XX BU-You
XX WPI; 2
XX Grant
PF Micros
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor (AAWI1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 kb fragment of the comprising DNA encoding the alpha-2B adrenceptor is deposited as C comprising DNA encoding the alpha-2B drenceptor is deposited as C CTCC 68144. Vectors have been adapted to allow prodn. of alpha-2B drenceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and bind to, the cells adrenceptor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies,
                                                                                                                                                                                                                                                                      Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target
                                                                                                                                                                                                              Claim 1; SEQ ID NO 1181; 65pp;
                                                                                                                                                                                                                                                                 polynucleotides
                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-352189/33.
                                                                                                                                                                                                                                                                                                                                                                                               Au-Young
                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-DEC-2002.
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                                                                                                                                                                                                                                                                                                                                                                                             Seilhamer JJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathway polynucleotide probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             population; cancer; adenocarcinoma; leukaemia; asthma; neuropathy; Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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Pred. No.
                                                                                                                                                                                                                English
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RESULT 12
ABZ42624C
ID ABZ426
XX ABZ426
XX ABZ426
XX ABZ426
XX OA-MAR
XX G prot
KW G prot
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide
                                                                                                                                                                        New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease
                                                                                                                                                        cancer or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2001; 2001WO-US50107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe of the invention.
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DB; ABP81780.
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Pred. No.
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Disclosure;

Fig 1; 523pp; English

The present invention describes antigenic peptides (I) comprising:

Claim 1; SEQ ID

No 28203; 103pp; English

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

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RESULT 13
AAS92399/c
ID AAS923
XX AAS923
XX DNA en
XX Human;
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XX Ho
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Best Local
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
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DB; ABG28212.
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                                                                                                                                                                                                                                                                                                                                 PT,
                                                                                                                                                                                                                                                                                                                                                                                                  HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                              Liu C,
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Matches
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Best Local :
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                            prostate
for detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate expression marker cDNA 7982.
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                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                          presence
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marker; gene; ss.
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94.7%;
                                          of prostate
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                                            cancer,
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                                          stage
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Claim 1; Page 1278; 11750pp; English.

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RESULT 15
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XX ABA12
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Best Local S
Matches 18
                                                                                                                                                                                          07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting in a patient;
(e) selecting a composition for inhibiting prostate car (f) assessing the prostate cell carcinogenic potential (g) determining whether prostate cancer has metastasize (h) assessing the aggressiveness or indolence of prostate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient;
(I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human nervous system related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
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                                                                                                                                                                                                                                                                                                                                         18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic; neuroprotective; cytostatic; dermatological; virucide;
suppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
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                                                                                                                                                                   2000US-0215135.
2000US-0216647.
2000US-0216880.
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                                                                                                               2000US-0217487.
2000US-0217496.
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2000US-0190076
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                                                         2000US-0220963
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The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating cmedical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune theroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing, (e) neurological disease e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.
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P-PSDB; ABB15872.
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2000US-0232398. 2000US-0232399. 2000US-0233400. 2000US-0233401. 2000US-0233063. 2000US-0233064. 2000US-0233065.

2000US-0234997 2000US-0234998 2000US-0234223 2000US-0234274 2000US-0232080. 2000US-0232081. 2000US-0231968. 2000US-0232397.

2000US-0231413 2000US-0231414 200005-0231244

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2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231243.

2000US-0225758. 2000US-0225759. 2000US-0226279. 2000US-0226681. 2000US-0226868. 2000US-0227182. 2000US-0227109.

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2000US-0228924. 2000US-0229287. 2000US-0229343.

2000US-0229344

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CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 990 BP; 193 A; 336 C; 270 G; 188 T; 3 other;

Query Match 78.1%; Score 16.4; DB 22; Length 990; Best Local Similarity 94.4%; Pred. No. 2e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGCCCCACCATGGTCGGG 20

Qy 3 AGCCCCACCATGGTCGGG 20

Db 563 AGCCCCACCATGGTCGGG 580

Search completed: February 12, 2004, 04:01:27

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Query Match Best Local Similarity

100.0%;

Score 21; DB 4; Pred. No. 0.18;

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OUT 1 09-016-434-1181/c equence 1181, Application US/09016434 atent No. 6500938 APPLICANT: Janice Au-Young APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION TITLE OF INVENTION: COMPOSITION FOR THE DETECTION UMBER OF SEQUENCES: 1490 CORRESPONDENCE ADDRESS: ADDRESSEE: INCTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: FIDAPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6 CURRENT APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH CLASSIFICATION: APPLICATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-0002 US TELLEDHONE: (650) 845-4166 INFORMATION FOR SBQ ID NO: 1181: SEQUENCE CHARACTERISTICS: LENGTH: 2072 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: Linear IMMEDIATE GOURCE: LIBRARY: GENBANK	ALIGNMENTS	09-252-9 09-252-9 09-252-9 09-252-9 09-252-9 08-073-3 08-254-3 08-481-C 08-481-C 08-754-6 08-754-6 08-756-3	69.5 1413 4 US-09-252-991A-
ON OF SIGNALING		Sequence 15698, Sequence 10, App Sequence 11, App Sequence 15622, Sequence 1769, Sequence 2, Appl	Sequence 15729

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Matches

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US-09-773-426A-13/C

Sequence 13, Application US/09773426A Patent No. 6534302

GENERAL INFORMATION:

APPLICANT: Tsia, Fong-Ying APPLICANT: Rudolph-Owen, Laura A. APPLICANT: Glucksman, Maria Alexandra APPLICANT: Williamson, Mark

Williamson, Mark Tsia, Fong-Ying

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TITLE OF INVENTION: 24438, 23553, 25278, and 26212 No. 6534302el TITLE OF INVENTION: Human Sulfatases (A CIP Application) FILE REFERENCE: 35800/208398(5800-79 CURRENT EPLICATION NUMBER: US/09/773,426A CURRENT FILING DATE: 2001-01-31 PRIOR APPLICATION NUMBER: US 09/495,823 PRIOR FILING DATE: 2000-01-31 NUMBER OF SEQ ID NOS: 14 NUMBER OF SEQ ID NOS: 14 NUMBER OF SEQ ID NOS: 14
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NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPHONE: 352-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
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APPLICANT: MacLennan,
Sequence 1, Application 05/092250, Patent No. 6518414
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                             Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Molecular Cloning and Expression TITLE OF INVENTION: G-Protein Coupled Receptors NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: Decemb CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                            Local Similarity
les 17; Conserv
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                                                                                                                                        139 AGCCCCACCATGGGCGGTT 157
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                                                   Application US/09225024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.2%;
89.5%;
                                                                                                                                                                                                                              75.2%;
89.5%;
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Pred. No. 70;
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                Score 15.8;
Pred. No. 70;
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1070 AGACCCACCAGGGTCGGGT 1052

AGCCCCACCATGGTCGGGT 21

US-08-196-989B-1 RESULT 3

Sequence 1, Application US/08196989B Patent No. 5585476

GENERAL INFORMATION:

APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

STREET: 2722 CITY: Gainesville

EL

NDDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1

COUNTRY:

SD

32606

INFORMATION FOR SEQ ID NO:

TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100 TELEFAX: 904-372-5800

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION UMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC

MAC-100

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION UNMBER: US/08/196,989B
PILING DATE: 15-FEB-1994

0

US-09-773-426A-13

Query Match

Local

ch 75.2%; 1 Similarity 89.5%; 17; Conservative

0; Mismatches

2;

Score 15.8; Pred. No. 6

66; DB SEQ ID NO 13 LENGTH: 1710 TYPE: DNA ORGANISM: homo sapiens

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APPLICANT: Williamoon, Mark
APPLICANT: Tsia, Fong-Ying
APPLICANT: Tsia, Fong-Ying
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22438, 23553, 25278, and 26212 No. 653
TITLE OF INVENTION: Human Sulfacases (A CIP Application)
FILE REFERENCE: 35800/208398(5800-79
CURRENT APPLICATION NUMBER: US/09/773,426A
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 09/495,823
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 14
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-773-426A-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-225-024-1
                                                SOFTWARE: FASTSEQ
SEQ ID NO 6
LENGTH: 2940
                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09773426A Patent No. 6534302 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                             APPLICANT: Glucksman, Maria Alexandra
             TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pair
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MO
TITLE OF INVENTION: G-
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PILING DATE: 15-FEE
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89.5%;
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G-Protein Coupled Receptors
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Pred. No. 70,
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; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; EATURE:
; PAAFE/KEY: CDS
; LOCATION: (23)...(154)
US-09-662-250A-10
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US-09-662-250A-10
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brett & MANNE APPLICANT: Jacqueline Wyatt TITLE OF INVENTION: ANTI-
FILE REFERENCE: RTS-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (334)...(2043)
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                       ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                     TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                     APPLICANT:
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Local Similarity 89.5%;
les 17; Conservative
              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            COUNTRY: USA
ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION
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                                                                                                                                                                                                                                 JAMES C. BRKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                 THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                GEORGE J. DAWSON
GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                                                                   ANTHONY SCOTT MUERHOFF
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brett P. Monia
                                                                                                                                                                                                                                                                                                                                                                              . SIMONS
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Pred. No. 87
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Pred. No. 70;
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                                                                                                                                                         D377/AP6D
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,260A

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                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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LENGTH: 369 base naive
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: POREMBSKI PRISCILLA I
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AAAGCCCCACCATAGGCCGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.4%; Score 15.2; DB 4; 1 Similarity 85.0%; Pred. No. 1.1e+02: 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08488446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
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JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
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THOMAS P. LEARY
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                                                                                   US/08/424,550
                                                                                                                                                  US/08/488,446
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HRR: 5527.PC.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6586568
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.0 Matches 17; Conservative
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                                                                                                                 TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,344A

FILING DATE: 07-Un-1995

CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA:

APPLICATION UNMBER: 08/424,550

FILING DATE: «UNKnown>
ATTORNEY/AGENT INFORMATION:

NAME: POREMBSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REGISTRATION NUMBER: 33,207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 5527.PC.01 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JAMES C. ERKER
SHERI L. BULJK
SHERI L. BULJK
ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C,
REAGENTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                   LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                               TELEPHONE: 708-937-6365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
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TAMI J. PILOT-MATIAS
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GEORGE G. SCHLAUDER
SURESH M. DESAI
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ANTHONY SCOTT MUERHOFF
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Pred. No. 1.1e+02;
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FOR THEIR USE
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SEQ ID NO:

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RESULT 11
US-09-149-476-36/c
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                  EARLIER
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al. TITLE OF INVENTION: 186 FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
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                                                                                                    FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/047,597 FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/047,615 FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/040,163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 1997-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/038,621 FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,878
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,662
ER FILLING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,882
ER APPLICATION NUMBER: 60/056,882
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,637
             ER APPLICATION NUMBER: 60/056,911
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,636
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,874
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,910
ER APPLICATION NUMBER: 60/056,910
ER FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ER FILING DATE: 1997-04-11

RE APPLICATION NUMBER: 60/043,313

RE FILING DATE: 1997-04-11

RE APPLICATION NUMBER: 60/043,672

RE FILING DATE: 1997-04-11

RE APPLICATION NUMBER: 60/043,315

RE APPLICATION NUMBER: 60/043,315
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RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,612
RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,632
RR APPLICATION NUMBER: 60/047,601
RR APPLICATION NUMBER: 60/047,601
                                                                                                                                                                            APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
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1997-08-22

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APPLICATION NUMBER: 60/047,590
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APPLICATION NUMBER: 60/056,892
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1 AAAGCCCCACCATGGTCGGG 20
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PLICATION NUMBER: 60/056,845
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CCATION NUMBER: 60/043,576
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85.0%;
                            Score 15.2; D
Pred. No. 1.2e
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                                                           DB 4;
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US-09-252-991A-4200/c
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4268
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SEQ ID NO 4484
                                  GENERAL INFORMATION:
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SEQ ID NO 4268
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Best Local Similarity
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 APPLICANT: Marc J. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 6 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-252-991A-4484
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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6551795
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                Conservative
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Rubenfield et
NUCLEIC ACID
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Pred. No. 1.2e
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Pred. No. 1.2e+02;
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 AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Sequence 1, Application US/09050861B

Patent No. 655314

GENERAL INFORMATION:
APPLICANT: Bayan, Donald

TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING
FILE REFERENCE: RIGL-002CON

CURRENT APPLICATION NUMBER: US/09/050,861B

CURRENT FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: US/09/651,150B

PRIOR FILING DATE: 2000-08-30

PRIOR FILING DATE: 2000-08-30

PRIOR FILING DATE: 1998-03-30

NUMBER OF SEQ ID NOS: 35

SOPTWARE: PATENTING DATE: 1998-03-30

NUMBER OF SEQ ID NOS: 35

SOPTWARE: PATENTING DATE: 1998-03-30

NUMBER OF SEQ ID NOS: 35

SOPTWARE: PATENTIN VERSION 3.1

ENGTH: 1911

TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4200
SEQ ID NO 4200
LENGTH: 1611
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4200
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Search completed: February 12, 2004, 06:07:49 Job time: 30.6829 secs
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US-09-050-861B-1/c
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                                                                                                                                                                                                              72.4%; Score 15.2; DB 4; Length 1911; Local Similarity 85.0%; Pred. No. 1.3e+02; les 17; Conservative 0; Mismatches 3; Indels 0;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/pcr_i
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-6/ptodata/1/pubpna/USO6_PUBCOMs.seq:*
-6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
-6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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US-09-825-923-3

US-10-077-870-3

US-10-010-073-1

US-10-305-720-1181

US-10-225-5678-41

US-09-918-995-29585

US-09-918-995-29585

US-10-027-632-131352

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US-10-001-073-2
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                                            Sequence 14, Appl
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Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1181, Appli
Sequence 41, Appli
Sequence 41, Appli
Sequence 41, Appli
Sequence 29585, A
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Sequence
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75.2	75.2	75.2	75.2	75.2	75.2	75.2	75.2	75.2	75.2	75.2	75.2	75.2	76.2	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	78.1	78.1	78.1
1710	1710	1710	1615	1615	1615	1290	1290	1290	1287	716	716	638	1446	7193	7193	7193	7193	1182	1182	1182	1182	1134	607	607	607	607	35178	28438	6997
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US-10-314-881-13	US-10-345-680-15	US-10-426-776-16	US-10-074-095-1074	US-10-212-872-1074	US-09-764-860-1074	US-10-369-493-38181	-10-369-49	US-10-369-493-35369	-10-369-493	-10-027-63	-10-027-632	US-10-198-846-4384	1	-086	US-10-288-985-1	338-	US-10-214-519-1	US-10-289-980-6	US-10-288-985-6	US-10-071-338-6	US-10-214-519-6	US-10-084-817-279	US-10-027-632-139092	6	US-10-027-632-139092	US-10-027-632-139091	US-10-017-161-739	US-09-820-790-3	US-10-094-886-137
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ALIGNMENTS

RESULT 1 US-10-001-073-14

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Sequence 14, Application US/10001073
Publication No. US2003013725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
ITILE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT FILING DATE: 2001-11-01
CURRENT FILING NAME COCCACCATGGTCGGGT 21
CURRENT FILING DATE: 2001-11-01
CURRENT FILING NAME COCCACCATGGTCGGGT 21
CURRENT FILING NAME COCCACCACGATGGTCGGGT 21
CURRENT FILING NAME COCCACCACGATGGTCGGGT 21
CURRENT FILING NAME COCCACGATGGTCGGGT 21
CURRENT FILING NAME COCCACGATGGTCGGGT 21
CURRENT FILING NAME COCCACGATGGTCG
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; ORGANISM: Rattus norvegicus
US-09-908-975-4848
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                                                                      Query Match
Best Local S
Matches 21
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Best Local :
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
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NUMBER OF SEQ ID NOS: 10
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APPLICANT: Heinonen, Pa
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                                                                                                                                                              NAME/KEY: CDS.
LOCATION: (11). (1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                ENGTH: 1344
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 686 AAAGCCCCACCATGGTCGGGT 666
                                                                                           Similarity
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                       AAAGCCCCACCATGGTCGGGT 21
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Salonen, Jukka T
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Alhopuro, Pia
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                                                                          Conservative
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US-09-825-923-3/c

GENERAL INFORMATION:

APPLICANT: Snapir, Amir

Heinonen, Paula Alhopuro, Pia

Karvonen, Koulu, Markku

Matti

APPLICANT: APPLICANT:

Pesonen, Ullamari

Sequence 3, Application US/09825923 Patent No. US20010016338A1

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CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LEGGTH: 1344
TYPE: DNA
ORGANISM: Homo Bapiens
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APPLICANT: Salonen, Jukka T
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
FULRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION UNMBER: FI 20010323
PRIOR APPLICATION UNMBER: FI 20110323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
NUMBER: Patentin Ver. 3.1
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Publication No. US20030113725A1
GENERAL INFORMATION:
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                                                                          Matches
                                                                                          Query Match
Best Local Similarity
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
FILE REFERENCE: 17070 NUMBER: 110/10/001.073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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686 AAAGCCCCACCATGGTCGGGT
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Similarity 100.0%;
21; Conservative 0
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Pred. No. 1.4;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
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APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
RUMBER OF SEQ ID NOS: 10
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NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
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NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                  LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1353
                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                            989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          686 AMAGCCCCACCATGGTCGGGT 666
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                                                                                                                           1 AAAGCCCCACCATGGTCGGGT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Ver. 2.1
                                                                                          ANAGCCCCACCATGGTCGGGT 666
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Salonen, Riitta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scheinin, Mika
Salonen, Jukka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                             Conservative
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                                                                                                                                                             <u>,,</u>
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Pred. No. 1
                                                                                                                                                                            Score 21; DB Pred. No. 1.4;
                                                                                                                                                           Mismatches
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                                                                                                                                                                                              DB 15;
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                                                                                                                                                                                              Length 1353;
                                                                                                                                                             Indels
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-1
                                                                                                                                                                                                                    Sequence 41, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
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Tocal Similarity
Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR PILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
FURRENT FAPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
                                                                                                                                  APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
                                                                                                           APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glerna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 100
21; Conservative
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100.0%; Pred. No. 1.4;
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Pred. No. 1.3;
0; Mismatches
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NUMBER OF SEQ ID NOS:

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US-09-918-995-29585/c
; Sequence 29585, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID
; TITLE OF INVENTION: FROM VARIOUS CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-814-353-19559
                                                                                                                              RESULT 12
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PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PRILICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
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SEQ ID NO 41
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 19559
                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                         Matches
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREV
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, John APPLICANT: Thompson, APPLICANT: Lillie,
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                            LOCATION: 4327, 4328, 4329, 4330, LOCATION: 4337, 4338, 4339, 4340, LOCATION: 4337, 4348, 4349, 4350

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/257,672
FILING DATE: 2000-12-21
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Pred. No.
                                                                                                                                                                                                                                                                          Score 16.8; DB 1:
Pred. No. 1.3e+02
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4341, 4342, 4343, 4344,
       SEQUENCES OBTAINED LIBRARIES
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1.3;
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4345,
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(481)
; OTHER INFORMATION: n = A,T,C
US-09-918-995-29585
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US-10-027-632-131352/c
片
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US-10-027-632-131352
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 131352
LENGTH: 565
                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 20411-756
                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/156,358
  551
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l Similarity 94.4%;
17; Conservative
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                                                                               l Similarity
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  AGCCCCACCATGCTCGGG
                                      AGCCCCACCATGGTCGGG 20
                                                                               Conservative
                                                                                                                                                                                                                                                                  for Windows Version 4.0
                                                                                                                                                                                                                                                                                                          1999-08-09
                                                                                                     94.4%;
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Pred. No. 2.3e+02;
  534
                                                                                 <u>,,</u>
                                                                                                       Score 16.4; DB 13
Pred. No. 2.3e+02;
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                                                                                   Mismatches
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                                                                                                                            DB 13;
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                                                                                                                          Length 565;
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RESULT 14
US-10-027-632-131352/c
US-10-027-632-131352, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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LENGTH: 565
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-131352
Search completed: February 12, 2004, 06:15:44
Job time : 128.341 secs
                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 38
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-891-38
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US-10-220-891-38/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/220,891
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: JP 2000/140387
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: JP 2000/159195
PRIOR APPLICATION NUMBER: JP 2000/159195
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 1108
SOFTWARE: Patentin version 3.2
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PRIOR FILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR PILLING DATE: 2000-03-29
PRIOR PILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR PILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131332
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                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWARA, AKIRA
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERITICS OF ENHANCED
TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
FILE REFERENCE: 7388-73435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                       Y Match 78.1%; Score 16.4; DB 13; Length 2262; Local Similarity 94.4%; Pred. No. 2.1e+02; hes 17; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                  3 AGCCCCACCATGGTCGGG 20
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1487 AGCCCCACCATGCTCGGG 1470
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21
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261
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AW391095
AI582395
AU166948
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BQ880026 AGENCOURT
AW391095 MR3-ST020
AI582395 tr97b09.x
AU166948 AU166948
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AA448314 zw96h03.s	AA448314	9	448	78.1	16.4	45	
BI713098 ie02b10.y	BI713098	12	446	78.1	16.4	44	(1
AA447622 zw97b03.s		9	442	78.1	16.4	43	
zw96h03		φ	433	78.1	16.4	42	()
		10	430	78.1	16.4	41	
zw97b03.r	₿	9	379		16.4	40	()
~	_	14	365	78.1	16.4	39	()
BY200267 BY200267		13	360	78.1	16.4	3 8	
BY337375 BY337375	ш	13	354	78.1	16.4	37	
BY214037 BY214037	-	13	345	78.1	16.4	36	
BY195012 BY195012		13	341	78.1	16.4	35	
BY149362 BY149362		13	333	۳.	16.4	34	
BF811542 CM2-CI017		10	333	8	16.4	ω G	
BF946030 CM0-NN115		10	212	78.1	16.4	32	
BG242458 602354253		10	1146		16.8	<u>ω</u>	
BU587459 AGENCOURT		13	1059	0	16.8	30	
BQ061158 AGENCOURT		12	1029		16.8	29	()
BZ551182 pacs1-60_		29	957	0	16.8	28	
AL533975 AL533975		9	950		16.8	27	
AL549851 AL549851		9	946		16.8	26	(3
BF307809 601890896	BF307809	10	912	80.0	16.8	25	()
BU603088 AGENCOURT		13	896		16.8	24	(1
AL223914 Tetraodon		29	894		16.8	23	
BH794448 ME_MBa000		28	726		16.8	22	
CB529586 UI-H-FT2-	CB529586	14	697	80.0	16.8	21	
u70g04.x		φ	659		16.8	20	
CA912228 PCSC21166		14	492		16.8	19	()
AI494022 gz97h04.x		ø	449	80.0	σ	18	
BX316223 BX316223		13	407		16.8	17	
BY401935 BY401935		13	376		σ	16	()
BQ053165 AGENCOURT		12	1017	_	17	15	()
BM469354 AGENCOURT		12	960	_	17	14	()
BP111519 BP111519		12	703	-	17	13	(3
AZ571445 287PvG04		28	696	_	17	12	()
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AI216547 qm36h04.x		ø	212		17.4	œ	()
AGENCO	BQ9238	13	956		17.8	7	.,
AL566688 AL566688	AL56668	9	921	84.8	17.8	σ	
AI419320 tf27e11.x	AI419	9	724	84.8	17.8	σ	

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ALIGNMENTS

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RESULT 1
BQ880026/c
LOCUS
LOCUS
ACENCOURT 8113358 Lupski_dorsal_root_ganglion Homo sapiens cDNA
Clone IMAGE:6179035 5', mRNA sequence.

ACCESSION
B0880026
REST.
ACCESSION
RESTON
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens (human)
ORGANISM
ELKARYOCE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution can be
found through the I.M.A.G.E. Consortium (LLNL)
brary Limses Procure Sisselence Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM13559 row: i column: 20
High quality sequence stop: 430.

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FEATURES
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AW391095
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 bp mRNA linear
MR3-5T0203-131299-111-f11 ST0203 Homo sapiens cDNA,
AW391095
                                                                                                                                                                                                   High quality sequence start: 10 High quality sequence stop: 63. Location/Qualifiers
                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-ST0203-
131299-111-fl1&t3=1999-12-13&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3P http://www.ludwig.org.br/ORESTES.
                                                                                                                                                                                                                                                                     primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

1 334 c 345 g 183 t
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/clone lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/noti; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
Si-TCGACCCAGCGGTCCG-3' and
Si-TCGACCCAGCGGTCCG-3' and
Si-TCGACTAGATCGCGAGCGGCCGCCCT[15]-3'. Size selected >
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'sex="male"
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clone="IMAGE:6179035"
                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
                                                                   /dev_stage="Adult"
/clone_lib="ST0203"
                                                                                                           db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thmor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1875 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 269)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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larity 95.0%;
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                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2227001"
/tlssue_type="adenocarcinoma"
/lab_host="DH10B"
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80 g 60 t
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cDNA clone IMAGE:2227001
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Rice callus (2001) Oryza

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mRNA sativa

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cultivar-group)

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Bonaldo, Ph.D.

CONA Library Arrayed by: Greg Lennon, Ph.D.

CNA Sequencing by: Washington University Genome !

Clone distribution: NCI-CGAP clone distribution

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html
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1 (bases 1 to 724)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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Contact: Takuji Sasaki
Continal Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.

1 (Dases 1 to 376)
Sasaki, T. and Yamamoto, K.
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AU166948
AU166948.1 GI:12405347
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similar to gb:X52255_rna1
                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-298-38-7441
Fax: 81-298-38-7468
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                                                                                                                                                                                          cgapbs-r@mail.nih.gov
Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="C60162"
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/clone_Tib="Rice_callus (2001)"
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Homo sapiens cDNA clone IMAGE:2097452
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cgi-bin/cluster.cgi?seq=CSODF019DD06NP1&cluster=8536.r. Contact cgi-bin/cluster.cgi?seq=CSODF019DD06NP1&cluster=8536.r. Contact cgi-bin/cluster.cgi?seq=CSODF019DD06NP1.
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600 http://fulllength.invitroden Corpor
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8536.r
more information about this cluster, see
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AL566688 Homo sapiens FETAL BRAIN Homo
CSODF019YH12 3-PRIME, mRNA sequence
AL566688
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Full-length cDNA libraries and normalization
Unpublished
On Feb 16, 2001 this sequence version replaced gi:12919302.
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1 (bases 1 to 921)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone="Organ: brain; Vector: pCMVSPORT_6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="glioblastoma (pooled)"
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/mol_type="mRNA"
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14009 row: g column: 22
High quality sequence stop: 413.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Tissue Procurement: ATCC
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184 c 269 g 176 t 61 others
                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:6473613"
/tissue type="letomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH1M MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 2.1 kb. "
a 248 c 228 g 233 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Insert Length: 589 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 177.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                          A1869725 A1869725 A1869725 A1869725 A1869725 A1869725 A198h12.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2432999 3' similar to gb:L11285 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE (HUMAN);, mRNA sequence.
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.,
                                                                                                                                                                                                                                                                                                                                  AI869725.1 GI:5543693
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/clone libe NCI CGAP Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a /note="Torgan: lung; Vector: ptr7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

a 51 c 60 g 48 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db xref="taxon:9606"
'clone="IMAGE:1883959"
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Pred. No. 1e+03;
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            R. Rosenfeld M.D.,
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740 bp DNA linear GSS 02-APR-20
ME MBa0003L01r Manihot esculenta Manihot esculenta genomic clone
ME_MBa0003L01r, genomic survey sequence
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BH794919
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                                                                                                                                                                                                                                                                                New Genomic Resources for Cassava (Manihot esculenta): Development of a Deep-Coverage BAC Library and Preliminary STC Analysis
                                                                                                                                                                                                                                                                                                 1 (bases 1 to 740)
Tomkins, J.P., Fregene, M., Main, D., Goicoechea, J.L., Blackmon, B., Atkins, M., Tohme, J. and Wing, R.A.
New Genomic Resources for Cassava (Manihot esculenta): Developme
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Euphorbiaceae; Manihot.
                                                            Email: jtmkns@clemson.edu
Total High Quality bases = 176
Total High Quality bases = 176
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                         Tel: 864 656 6419
Fax: 864 656 4293
                                                                                                                                                                            Clemson University
100 Jordan Hall, Clemson University, Clemson,
                                                                                                                                                                                                                    Contact: Tomkins J
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                          Manihot esculenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manihot esculenta (cassava)
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High quality sequence stop: 364.
Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1703 Std Error: 0.00
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quality sequence start: 38 quality sequence stop: 514. Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH108"
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Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11902 row: g column: 05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1485 bp
603314820F1 NCI_CGAP_Mam6 Mus mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1485)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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    /db_xxef="tax".
/db_xxef="tax".
/db_xxef="tax".
/db_xxef="tax".
/db_xxef="tax".
/dcone="IMAGE:5354908"
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/tissue_type="infiltrating ductal carcinoma"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/dev_stage="5 months"
/lab_host="DH10B"
/clone lib="NCI CGAP Mam6"
/clone lib="NCI CGAP Mam6"
/note="Oxgan: mammary; Vector: pcMV-SPORT6; Site 1: Sall;
/note="Oxgan: mammary; Vector: pcMV-SPORT6; Site 1: Sall;
/site_2: Noti; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
07 a 342 c 327 g 306 t 3 others
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a 216 c 158 g 191 t 1 othe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Manihot_esculenta"
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
analysis see
                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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To order clones from this library see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Manihot
/mol_type="genomic
/strain="MECW72"
                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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/clone="ME_MBa0003L01r"
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Query Match

82.9%;

Score 17.4;

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Length 1485;

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EST 11-FEB-2003

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AZ571445/c
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2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
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Carlton, J.M.-R. and Dame, J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
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Dept. of Patholiclogy, College of Veterinary Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Seq primer: M13(-20) forward
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                                                                                                                   Conservative
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                                                                                                                                                                                                                                       g)
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/mol_type="genomic DNA"
/strain="Salvador I (Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dev stage="asexual blood forms"/lab_host="Saimiri boliviensis"
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BP111519 ORCS bovine utero-placenta
ORCS11942 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This work was performed to collaborate with Developmental Biology Department, National Institute of Agrobiological Sciences. Address: 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax: 81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System (ORCS) project of Ministry of Education, Culture, Sports, Science and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Gozoh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
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This work was performed to c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 960)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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D
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/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="ORCS11942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mixture of uterus and placenta"
/dev_stage="adult"
/clone_lib="ORCS bovine utero-placenta cDNA"
152 c 203 g 183 t 2 others
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                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2121 row: g column: 23
High quality sequence stop: 825.
Location/Qualifiers
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AGENCOURT_6821899 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5934766
5', mRNA sequence.
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1 (bases 1 to 1017)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 545.
Location/Qualifiers
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Plate: LLAM12265 row: e column: 19
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/tissue_type="lymphoma, cell line"
/lab_host="DH108 (phage-resistant)"
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/clone_lib="NIH_MCC_85"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 221 c 248 g 241 t
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
                                                                             clone="IMAGE:5934766"
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                                                                                                                                                                                 .1017
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279 þ /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT ORIGIN

Matches Query Match Best Local (Similarity Conservative 100.0%; 81.0%; Score 17; DB 12; Length 1017; 100.0%; Pred. No. 2e+03; 0, Mismatches 0 Indels 0, Gaps 0

밁 ঠ 1004 AAAGCCCCACCATGGTC 988 1 AAAGCCCCACCATGGTC 17

Search completed: February 12, 2004, 06:05:52 Job time : 1142.79 secs

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Minimum DB
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is the number of results predicted by chance to have a

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Liggett, S.B. and Small, K.M. Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 15 25-OCT-2001;

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RS. Mizny, D. Marie, Metzker, M.Lee., Adams, C., Allen, C., Allen, H., Algbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Baca, E., Bandaranaike, D., Biawalo, K., Blair, J., Blankenburg, K., Blyth, P., Barden, R., Carter, K., Cavazos, I., Cearch, P., Burrell, K., Calderon, E., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Cleveland, C., Coxteall, R., Cox, C., Coyle, M., Cree, A., Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., DeJgado, O., Denson, S., Dugan, Rocha, S., Dunn, A., Durbin, K., Eaves, K., Egan, A., Escotto, M., Eugene, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagy, N., Flagy
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                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Chriattoideae; Oryzae; Oryza.

I (bases 1 to 154555)

Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L.L., Telttrin, T., Kim, M.M., Bera, J.J., Jin, S.S., Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V., Vanaken, S.S., Riedmuller, S.B., Peterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.

Oryza sativa chromosome 3 BAC OSJNBa0059E14 genomic sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30040 CTGATTGCCAAACGAGCAA 30058
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Submitted (24-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Sequencing is completed to a minimum standard of double strand Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 3 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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                                                                                                                                        Direct Submission
Submitted (15-APR-2003) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
4 (bases 1 to 154555)
                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-NOV-2002) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 154555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence. AC135958
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Medical Center Dr, Rockville, MD 20850, USA, ri
On Apr 15, 2003 this sequence version replaced
Address all correspondence to:rice@tigr.org
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                                                                        Submitted (25-APR-2003) The Institute for Genomic Research,
                                                                                                                        Buell, R
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                                                                                                Direct Submission
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/mol_type="genomic DNA"
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10970 c 10929 g 1
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94.7%;
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                          rbuell@tigr.org
ed gi:24462343.
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clone OSJNBa0059E14 is from Oryza sativa orientation of the sequence is from SP6 t

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FEATURES
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                                                                                  repear_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This BAC overlaps with rice BAC OSJNBb0015102 (AC135563). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="OSJNBa0059E14.1"
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complement (join(<2338. .2570,2665. .>3123))
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complement (join(2499. .2570,2665. .3123))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="j
                               /rpt_family="(CGG)n"
9301..11079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAAIANLELSTHTHTHTQRVCSIDRPSPRAHDGERSSQPRRGGG
GDRGVCGCRGGGGGRRGRGGGVVRRRGERAGAVRAVPAGRRGAAGRSVLRRREGAARD
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/gene="OSJNBa0059E14.2"
/gene="OSJNBa0059E14.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="AT_rich" complement(2338. .312
                                                                                                                     KCRETKARSCLRKLLRNFRLRFKL"
                                                                                                                                                                              , t tänslation" mrimvrtikggrvaldvogatttvaqvkgmvareriavamorl
fragrclddhrtladygvrhdsvverlslilatdaygvemhnymelmopetatakoemh
Qoqoqlihvhvaaddeekaikkkpverlalkilsrlovdawtsohdaktlolllrho
Gggggarnvgeltgedwssiraelnaatgsgfpveelorrlgefrrefeaasriknhp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unknown protein"
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                                                                                                                                                    rfsydprrrvvvakQadwknyilenpeaaayegrsprhlgrlraifsgdgggggggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="0SJNBa0059E14.1"
(codon Btart-1
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/cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mote="highly similar to cellulose synthase catalytic subunit GB:AAC3936 GI:2827143 (Arabidopsis thaliana); EST AU064228, AU176399, CB096725, AA751514 from this gene" join(15663...16059,16193...16379,16712...16962,17065...171243...17429,17725...17991,18085...18430,18519...18656, 18739...18864,18950...19162,13222...19577,19773...19975, 20219...20569,20652...>21236)
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13913
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LAGFGVVNNTFAALEAPYCDETSRVDARFAV FVGEVSQPSRAAAAVRRGGDGDVDCL
RWLSTKPSQSVVYVCFGSWAHFSVTQTTRELALGLEASNQPFLMVIRSDSGDGGGENE
PEGWERRMEGRGMVVRGWAPQLAVLAHPSVGAFVTHCGWNSVLEAAAAGVPALTMPLV
FEQFINERLVTEVAAFGARVWEDGGGKRGVRAREAETVPAGVIARAVAGFMAGGGGRR
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/rpt_family="(CCG)n"
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ERMLTWRWNSGRNDDIVHSKYDSGEIGHPKYDSGEIPRIYIPSLTHSQISGEIPGASP
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/gene="OSJNBa0059E14.4"
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/note="similar to immediate early salicylate induced
glucosyltransferase GB:AAB36653 GI:1685005 (Nicotiar
                                                                                                     GTS1APSEGRGVGDIDASTDYNMEDALLNDETRQPLSRKVPISSSRINPYRMVIVLRL
IVLCIFLHYRITNPVRNAYPLWLLSVICEIWFALSWILDQFPKWSPINRETYLDRLAL
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AVEVEATMAVTPANAAAIAATVAGNAAVRVVCYPFPDVGLARGVECLGAAAAHDTWRV
                                                                    RYDREGEPSQLAPVDIFVSTVDPMKEPPLVTANTVLSILAVDYPVDKVSCYVSDDGAA
                                                                                                                                                                                                                                                                                                 /product="putative cellulose synthase catalytic subunit"
/protein id="AAP21426.1"
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/protein_id="AAP21420.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains Pfam profile PF03763 (remorin, C terminal region); EST BE041106,041920,AU097433 from this gene"
REYEEFKVRVNALVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTE
                                                                                                                                                               DHMMSPVGNIGRRGHPFPYVNHSPNPSREFSGSLGNVAWKERVDGWKMKDKGAIPMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="OSJNBa0059E14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAP21423.1"
/db_xref="GI:30103010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="putative immediate-early salicylate-induced"
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/gene="OSJNBa0059E14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(9301. .10065,10558. .11079)
/gene="OSJNBa0059E14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 176534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC135242 176534 bp DNA
Oryza Bativa (japonica cultivar-group) chr
OSJNBA0070D14, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K., Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A., Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (Dases I to 176534)
3 (Dases I to 176534)
Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K., Shari, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A., Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (10-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian
Agricultural Research Institute, LBS Centre, New Delhi, Delhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K., Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A., Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence for Oryza sativa chromosome 11 Clone OSJNBa0070D14
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Agricultural Research Institute, LBS Centre, New Delhi, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singh, N.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                   n Feb 28, 2003 this sequence version replaced gi:27502456. NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10012, India
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provided by the submittor.
This sequence will be replaced
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 49567: contig of 49567 bp in length
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GSAPINLSDRLNQVLRWALGSVEILFSRHCPIWYGYGGRLKFLERFAYINTTIYPLTS
IPLLLYCILPAICLLTGKFIIPEISNFASIWFISLFLSIFATGILEMRWSGVGIDEWW
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REAMCFLMDPNLGRRVCYVQFPQRFDGIDRNDRYANRNTVFFDIDLRGLDGLQGFVYV
GTGCVENTFALYGYEPEIKQKREGYFSSLCGRKKITKKSKEKSTEKKSHKHVDSSVV
VFNLEDIEEGIEGSGFDDEKSLLMSQMSLEKRFGQSSVFVASTLMEYGGVPQSATPES
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/gene="OSJNBa0059E14.6"
/note="similar to polygalacturonase precursor GB:AC26512
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IPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQN
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94.7%;
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Pred. No. 1.5e+02;
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REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

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TITLE JOURNAL

ACCESSION VERSION KEYWORDS

RESULT 4 AC135242

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FEATURES
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Best Local :
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                                  sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1541)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Chamez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Chamez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                           Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYU58358
Drosophila melanogaster GH12788
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                      cdna@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                          This clone was sequenced as part of a high-throughput process to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-OCT-2001) Berkeley Drosophila Genome Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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148805
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/note="(japonica cultivar-group)"
38483 c 37230 g 49875 t 576 others
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/mol type="genomic DNA"
/db_xref="taxon:39947"
/chromosome="11"
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Location/Qualifiers
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97492: contrig of 47825 bp in length
97592: gap of unknown length
145324: contrig of 47732 bp in length
145424: gap of unknown length
148404: contrig of 3380 bp in length
148904: gap of unknown length
165731: contrig of 16827 bp in length
165831: gap of unknown length
165834: contrig of 10703 bp in length.
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; Pred. No.
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full length
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. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
REFERENCE
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ORGANISM
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VERSION
KEYWORDS
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F21B23
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                            MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, Washu, to pick the best candidates for sequencing.
NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                       University,
Submitted by
                                                                                                                                                                                                                                                                                                                                         Submitted (01-MAY-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress) 
Arabidopsis thaliana
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AF262038.1
                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana BAC F21B23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Longest ORF"
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EFSLGSDKRDNYKMMALCDLAMYIIDSKFSPFDGNTSTFSMPLALPEMYYKEPAVANF
QNNDYJIPLDVYTLGAKSTSKAAATAMTTSRAAVAPKRPAEQSIMDDENPQENNLFDN
IRAADTTEPMAKRTRAGAASAKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana Genome Sequencing Project
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                                                                                                                                                                                                                             Department of Genetics, Washington St. Louis, MO 63108, USA e-mail: rwilson@watson.wustl.edu
                                                                                                                                                                                                                                                                                               Genome Sequencing Center
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Ab_xref="FLYBASE:FBgn0033676"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CG17509"
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neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation). ocation/Qualifiers

gene CDS gene CDS source /translation="MYMAYGWPQVIPLLPGSCPSSQRVVYLKLAGRILLLVVSPSHLEL MGSSQV1YHHLSAFPSWWSLELQRVRIGKSYMEDDKSYMEEGEBLUQAWSDDAKLIAVL FGGAFSIGSHEPSDSWDDLLSYTLGHCLVSGVASPTLASDDKFSTNPALVQLELCTRS KLLFVLNSDGQLVVCSVNKKGLKYTESIRAEKKVGGDAVCASVASQQOILAVGTRKGM VELYDLSHSISLLRTVSLHDWGYSADYTGPVNNIAWTEDNSAFAVGWKSRGLAVWSVS GCRLMSTVQOIGLTSTSSEPKLNPKQDCKYEPLWSGTSALVGDBYGYRLFATEBASVDK GCRLMSTVQOIGLTSTSSEPKLNPKQDCKYEPLWSGTSALVGDBYGYRLFATEBASVDK ILAFSFGKCCLNRGVSGKTYVRQVSYISQNWPVQHVAASEDGKYLAVAGLHGLILYDI join(2429. .2626,2668. .2775,3508. .3920,4187. .4538, 4709. .4932,5136. .5331,5530. .5597,5670. .5844,5931. .5978, 6028. .6081,6258. .6437,6567. .6679,6803. .6985,7177. .7234, 7456. .7515,7615. .7656,7752. .7879,7977. .8112,8243. .8278, 8454. .8570,8662. .8724,8808. .8909) /gene="F21B23.3" AVSQYCALRLLQATLDESLYDLAGELVRFILLRSGRDIEQAPTESDSLSPKLLGFIJFG SSHKKSSLDKSSSPKEQSPHASVKSILESHASYLMSGKELSKLVAFVKGTQFDIVNF AAGLELIGQKLQMSELQMRLDAFELLAQMCSVKFKEMIVLLATLLQRSEVLYDIFRYD LRLMKAYSVTLESHLAFAHYHDLLQILEAKLSATSREESNRGSIS" PLGLLPNVGVVVGVSQRMSFSASAEFACFEPTPQAQTILHCLLRHLLQRDKNEEALLL AQLSAEKPHFSHCLEWLLFTVFDAEISRPNPNRNQISGPGHLKKLSLLRKACDLIKKF PEYYDVVVNVARKTDARHWADLFSAAGISTTLFEDCFQRRWYRTAACYILVIAKLEGV RFKKMRVFGDVSQEQQIHCKGLLMLGKIVVICNYIEASETYELLFYPRYHLDQSSLLC RKVLLGKMYMDVYQDYILVSYLFFFHYYHVKIYGELTPSSKADLQHLREGELDNDN EKSDLSDREPSRCLLIKGNGELSLLDLVDGRERELTDSVELFMVTCGQSEEKIYNLVEE LSSDLSDREPSRCLLIKGNGELSLLDLVDGRERELTDSVELFMVTCGQSEEKIYNLVEE complement (join (10977. .11226,11408. /gene="F21B23.5" complement (10977. .11830)
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gene

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/evidence=not_experimental /protein_id="AAF88004.1"

codon_start=1 note="contains

similarity

ç

aminocyclopropanecarboxylate

db_xref="GI:9502151"

VMSGGATGANETIMFCLADPGDAFLVPTPYYAAYVYIHTLLVFK"

16686)

CDS

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/note="similar to a large family of Arabidopsis thaliana salt inducible protein-like proteins; contains similarity to Pfam family PF01535 (Domain of unknown function), score=340.5, E=1.9e-98, N=2"
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25152. .25208,25625. .25735,26021. .26062,26667. .26942))
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LINTILCKSRVDEALEVFEQMEGKRTDDGNVIKADSIHFNTLIDGLCKVGRLKEAEEL
LYRNKLEERCVPNAVTYNCLIDGYCRAGKLFTAKEVVSRMKEDEIKPNVVTVNTIVGG
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EMLTDMEKEGKLOBSITVNTLISFGCHKDFSSVERMMEDGLDFYCKNNEKVV
AVGSGELDEALKLFKDMGLHSKVNPNTVINILINAFSKLGNFGQALSLKEEMKMKM
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AKSQSIKRESSLSLALQSVIEFAGSEPDFRDKLLFLYEIAKEKNIPLTIVATKLLIR
WFGRMGNVAQSVLVYERLDSMKKASQVRNVVVDVLLRNGLVDDAFKVJLDEMLQXESVE
PDNRITADIVLHEVWKERLLTEEKIIALISRFSSHGVSPNSVWLTRFISSLCKNARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPKUPAIGRALLFEYLIGLMLLKTVLVERKSINSVECTELEKEMMERKNKAWEERDMSE
KGTVEVLHKEGLEKPLMSFEKPKFDRNELMSSISKVKGSEKKLELVNSSHVELDFDDK
IHEIKVMARRAREIEAGIELNEKEKRDVNKETGDSDEDISIGSGKSLEPIDGLTHSVGD
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GVIQASDVTKOQLSMMKNSTGRKSRVLRSVKBAKEFLSRRSGEKELTQELSQMAQDSD
EIFPKQSDEERGVARKHKLVDKNKILELYRSEYNDELEMMKDEKLRDIVFCVRDNELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (27206. .29561)
/gene="F21B23.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains similarity to Pfam family PF00076 (RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)), score=42.1, E=1.3e-08, N=1"
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ELSESASSENTLTPSSEITSSQPKIVVEGSDGSVRPGKKSGKEYWQHTKKWSRGFLEL
YNAETDPEVKAVMRDMGKDLDRWITEDEIKDAADIMEKLPERNKKFMEKKLNKLKREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains similarity to Drosophila melanogasterspectrin beta chain (GB:AAA28399.1) and heparan sulfate-N-deacetylase/N-sulfotransferases"
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Complement(24152. .26942)
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/db_xref="GI:9502154"
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                                                                                                                                                                                              /gene="F21B23.2"
join(39785...39801,40280...40444,40500.
40816...40861,40959...41072,41156...4133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MENGEYVTHKDTSLLKFVSSSSSSSEEEFRFVSSIQNAILRLD"
                                                                                                codon_start=1
                                                                                                                            note="contains similarity to Pfam family PF00350 (Dynamin amily), score=29.7, E=4e-06, N=2"
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.41317,41364. .41443)
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                                                     Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovs http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a varia of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                 On Apr 1
Address
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Town, C.D., Haas, B.J., Wu, D., Maiti, R., Hannick, L.I., Chan, A.P., Tallon, L.J., Rooney, T., Utterback, T.R., VanAken, S.E., Feldblyum, T.V., White, O. and Fraser, C.M.
Arabidopsis thaliana chromosome 2 BAC F23H14 genomic sequence
                                                                                                                                                                                                                                                                                      Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or. On Apr 18, 2002 this sequence version replaced gi:6598619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG
http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
mpertea@tigr.org), searches of the complete sequence agains
                                                                                                                                                                                                                                                                                                                                                                          Medical Center Dr., Rockville, 3 (bases 1 to 91268)
Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                    clone F23H14 is from Arabidopsis thaliana chromosome 2
orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                  orientation
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YNYKRMMLKKKKKKKLNCIAANQDCEVDPKGDMTKIDLKDQGTNAVETGRSSKVVST
VPLHRSIFSPNGCDIQSSFKFMCSTYHLSHLSSCIHTLTNFFLLKMFVIVNLTLVDLP
GLTKYAVGNKAMMSSKAEARDQMPLVIQVLQFH"
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57055. .59355
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GGHRSVESLADEAGITDQAGSLLPAKDNRPSEDLD"
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/gene="F21B23.9"
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/gene="F21B23.9"
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/protein_id="AAF88008.1"
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                                                                                                             (Mark Borodovsky,
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repeat. 1437023 repeat repeat. Fig. 1.021. repeat. Fig. 1.021. repeat. rep	/rpt_family="Rf:Spacer between 25S and 18S rDNAs part of the 10.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs"	IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA repeat region 449502	region 447500 repeat /rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of -3.5 Mbp on chromosomes II and repeat	unit 18 10.5 kbp, 2 loc1 of ~3.5 Mbp on chromosomes II and IV, 670 copies#Rf;ATR0026 XS2322 X15550 10.5 kbp rDNA repeat"	<pre>/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat</pre>	A	/rpt_ramily="Rf:rDNA repeat of 18s rDNA, intergenic spacer, 5-8s rDNA, spacer, 25s rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and repeat.	spacer between 25S and 18S rDNAs" repeatregion 414. 503 repeat.	rnna the To.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic			the 10.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs" repeat.	region 802705 /rpt_family="Rf:Spacer between 25S and 18S rDNAs part of	/rpt family""Rf:Spacer between 25s and 18s rDNAs part of repeat, the To.5 kbp rDNA repeat#Rf:ATRO032 X15550 intergenic spacer between 25s and 18s rDNAs"	spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of -3.5 Mbp on chromosomes II and repeat IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA	repeat_region 1.88 / The family="Rf:rDNA repeat of 185 rDNA, intergenic repeat of 185 rDNA, interpretable repeat of 1	misc_feature 1. 9372 Falling Topon Time International Control Internationa		/organisms franticopes contrains /organisms	Location/Qualifiers 191868	<pre>kNASGAN-SE (Sean Eddy, http://genome.wusbi.edu/eddy/tRNASCAN-SE/). imple repeats are identified by repeatmasker (Arian Smit, ittp://ftp.genome.washington.edu/RN/RepeatMasker.html).</pre>	Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene	nctp://www.tugr.org/cun/tgn.sntml/. Annotated genes are named to ndicate the level of evidence for their annotation. Genes with imilarity to other proteins are named after the database hits
region 85219584 'rpt_family="Rf:Spacer between 25S and 18S rDNAs part of the T0.5 kbp rDNA repeat#Rf:ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs"			_region 4/824945 _region 4/824945 repeat#Rf.ATR0029 X52320 U43225 5.8S rDNA" _region 49465133		4782 4945 /gene="At2g01025"		_region		/gene="At2301015" 27064513 /gene="At2301015"	27064513	er, 5.8s rDNA, spacer, 25s rDNA, spacer, 15s rDNA, spacer, 25s rDNA, spacer, 15s rDNA, spacer, 25s rDN	repeat" _region 27069364 /rpt family="Rf:rDNA repeat of 18S rDNA, intergenic	unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II an IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA	region 20812139 /rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer 25S rDNA, spacer entire rej	repain 2079. 2139 _region 2079. 2139 _rpt_family="Rf:Spacer between 25S and 18S rDNAs part	unit is 10.5 kbp, 2 local of ~3.5 Mbp on chromosomes II and IV, 670 copies#Rf:ATR0026 X52322 X15550 10.5 kbp rDNA	_regrous _r/r213 rDNA repeat of 18S rDNA, intergenic	/rpt_f the 10 spacer	region 17692139	<pre>spacer, 5.8s rDNA, spacer, 25s rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II an tv 670 cories#Bpf.wrpnOpselver329 v16560 10 5 kbp rPNA</pre>	spacer between 25S and 18S rDNAS" _region 14611519 _region 1761. repeat of 18S rDNA, intergenic	the 10.5 kbp rDNA repeat#Rf.ATR0032 X15550 intergenic spacer between 25S and 18S rDNAs" region 1461. 1829	region 1459. 1519 /rot family="Rf:Spacer between 25S and 18S rDNAs part

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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-JAN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Biochemistry, Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, per de la control of Biochemistry, Biochem
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AL670007
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this contig is an assembly of BAC 14A6 from 1 to: 11263, and BAC
12H14 from 11264 to: 91436rev (strain OR74A); BAC clones are
available at the Fungal Genetic Stock Center http://www.fgsc.net
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups and V can be viewed at: http://mips.gsf.de/proj/neurospora.
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Unpublished
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/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic pacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat"
9195. .9372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|XS2322|X15550 10.5 kbp rDNA
                                                                                                                                                                                                                                                                               entry for analysis
                          complement (join (5919.
/gene="B14A6.010"
complement (join (5919.
                                                                                                                                                                                                                                                                               /note="overlap to BAC B1308 contig,
entry for analysis and annotation"
                                                                                                                                                                                                         product="tRNA-Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Neurospora crassa"
/mol_type="genomic DNA"
/db_xref="taxon:5141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                        'gene="B14A6.010"
                                                                                                                                                                   note="tRNA predict as a tRNA- Gln :
                                                                                                                                                                                                                                                                                                                                                                                               chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aign, V., Hoheisel, J., Brandt, P., Fartmann, B., Nyakatura, G., Mewes, H.W. and Mannhaupt, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:18376186
                                                                                                                                                                                                                                                                                                                                                              . 7884
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90.0%;
                                                                                                                                                                                                                                                     .5451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91436 bp
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.6185,6494.
                                                                      .6185,6494.
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   .7692,7761. .7803))
                                                                   .7692,7761.
                                                                                                                                                                                                                                                                                                                     please
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Neurospora.
                                                                                                                                                                               anticodon
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                                                                   .7803))
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KRAVEKSEAMNPSKPTKVEBETALPKVHVPTPOTAROKATAAADVEATKAAKKAAAKAAAA QEEQAQMDQQQQQETQKPKKKEKKYAPEAMIPTSRFVGNVGKTAGAALDTTGQVA KGVTDTVGGTALGGGGVGKTVGAAAGGVGDTLGAATGGLGKTVEGATGGLAKGGP LGAVGGLGEGLGQTVGGVGKGLGDTVGGTVGGTLGDTVGGFLGCKVGGLARGGAVTG ITGGLGDGVGKGLGQTVGGTVGGTVGGLGDTVGGTLGGUGGGGGGQRR" complement (5919 . .6185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MPTATTVKQPSAAVSSTPKVKKTTKTETTDGPKPVKEVKHRSS
STKPKSTPLAETTDNVVKKEVEAPLDENKLATTDHAVKKPTTSTSTPEKKKARVHS
SSTYPREVVSSSTKKPSTSGHTHAHTSTTKTSSHRPHTHLEBSSKHESTSSHRPGRH
HHAHHHHNPDGSLTRHGARATSSSIAKPLAPAKAFSPALDAEGNPKPNLRPATMTAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /traiblation="MSNQRNPSHSLLDVNSFCSDDQKSVQEARNHSTSSNAPTNHAYV IPAQRRAMTPSDTPSVSAALAILDWRRKAQTPTSNTRSATEPVLVTRSPSNSFRPMDS VQGLEBTFTAEEKVRAGFSWRYKGD IRNPKNSSLTAPDDNCALFLTNI PAGTTPKIV LDALGIHAPFGRVYATSI DAPTDGRYKKSACARITMFCREEAVHVFQFTTGGNLKIAGR TIAVVMNSNRSAPQTTDLPHSASRVLEILGPIEVVDIHRLSRFLGANIKFDTQDVTTVR EDKOERLLRWTFCSFRAQAQVARKALRAEWPGLHIRWGIDPMAVSVNNVPTAMSTMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (7693.
/gene="B14A6.010"
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/protein_id="CAD21303.1"
/db_xref="GI:18376187"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [GGGGVGKT][ATGGLGKT]
contains EST gb:AW717407, AW708782"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (7761.
/gene="B14A6.010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (6494.
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DFYDAFVS RRGLENTRDRAEHTRKRKI VSHTFSAKSVQQFEPYMHSNLELFVKQWDS
MIKNSKNPDKAAHLDCLEWFNYLAFDV IGDLSFGQPFGMLSSGADMAE I RSSPDAAP I
YAPA I E I LNRRGEVSATLG I HPALKPFAKYLPDPFFTKGLAAVENLAGI A I ACVKSRL
                                                                                     /protein_id="CAD21305.1"
/db_xref="GI:19376189"
/taanslation="MAIISILMSPWAPVVLLAGVAFYYLVPYEVTYSALRKIPSBFPA
QFTDLWLLSVCRRGNRYQRVDELHKKLGPVVRIQPNHVSICDDAAIFTIYGHGNGFLN
                                                                                                                                                                                                                                                                                                                     /note="strong similarity to benzoate 4-monooxygenase (EC 1.14.13.12), Aspergillus niger, PIR:S12015 Contains Cytochrome P450 cysteine heme-iron ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join (13804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13804. .15397
/gene="B14A6.030"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFPQQRAPVATSEVSHTPAGDLISFDSDVEEGLDSKEEKSDIYDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="hypothetical protein"
/protein_id="CAD21304.1"
/db_xref="GI:18376188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="B14A6.010"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join (13804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="tRNA-Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="B14A6.020"
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                                                                                                                                                                                                                                                                                            signature [FSHGPRSCVG]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="B14A6.020"
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                                                                                                                                                                                                                                                                                                                                                                                                              gene="B14A6.030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="B14A6.030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="tRNA predict as a tRNA- Thr : anticodon agt"
                                                                                                                                                                                                                               product="probable benzoate
                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7692)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  .15031,15093.
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                                                                                                                                                                                                                                  4-monooxygenase cytochrome
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                                                                                                                                                                                                 20645. .20730
/gene="B14A6.050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVTTPQAVATADVRKELNFCTKTNIRVLGVVENMCGFVCPNCSECTNIFMSGGGEVMA
NDFGVRFLGRVPIDPQFLVLIETGKRPTYPAGTTVDGKDISTPAGASTSEEEEVKDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLTGPSIPRMFGIEDAKVTQAPGGWLPITVHEADPSAGVGSLRVMSLGFLLPKRGDAV
VWRGPKKTAMVRQFLSDVFWDETDYLLIDTPPGTSDEHISLAENLLQKARPGQLAGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similarity to putative nucleotide binding protein, Homo sapiens, TREMBL:AF118394_1 Contains ATP/GTP-binding site motif A (P-loop) [GKGGVGKS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="B14A6.050"
join(20612..20644,20731..21612)
/gene="B14A6.050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (17314.
/gene="B14A6.040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLPDLSYMLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPVSTLTSTRGPNPGTTTAEYMSQSDHVPVSLTLTSNLENNTTVPVTSSAADPWASAD
FSFFELPSQQQIGPTKSSVTPSRPSSMIATSFAPTAPGSSTHSFDLPRVTTPISSASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVSDHIITDSFNSISERKAWYRISRFGSSRKHNAGDDENYRRVAWPTSTVCQETLQTV
RRWMEEDSIAGRVSLGGGISKTQKNMFGWDSSAEPVTLDAIFGKRAVPTRPSSVQPLQ
PPSAFNLVDHSPLGSTAVNSLKWQPHRPASLQLPPAATFSWSSDFSASAGKPPLTASL
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GPPVIRRAESKSSLGPHHHDVSEEASDFGDFEDAQVKEPPSSQTPEPPSTPSEVQKPS
SQH&SSPTTSPTQSMSSQLGHMNELAAKFGALNFDIDLSNVDKMFETSTNMKPLFPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPAITAPSPWADAEDGFGGWAAPDGLTTQTATTAQSAWMGGWRSRSPSLAAPSRDNGF
RSRSPSLVAPSRENSWRSRSPSLIAPSRDNGFRSRSPSLAASVRDEEFAKSNPIAWPD
TIASSNSPIAPVLRQPSPDFWAAEHSHTPHNDDNITPRLVINLPQSIAEEEDDVDKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOHEA GRANDER CONTROL OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="B14A6.040"
complement(17314. .19917)
/gene="B14A6.040"
complement(17314. .19917)
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/db_xref="GI:18376191"
/translation="MSLAKWHIVLVLSGKGGVGKSSVTTQLALSLSLAGHSVGVLDV
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                http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/bsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of three methods: Gene genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-JAN-2001) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Jan 24, 2001 this sequence version replaced gi:12280869. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin,X. and Kaul,S.
Direct Submission
Submitted (28-SEP-1999) The I.
Medical Center Dr, Rockville,
3 (bases 1 to 96232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC clone T22K18 is from Arabidopsis chromosome III and is near the molecular marker CIC5D8.

The orientation of the sequence is from SP6 to T7 end of the BAC
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Washington), Genscan (Chris Burge,
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http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
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,C.Y., Utterback,T.R., Barnstead,M.E.,
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e, MD 20850, USA, xlin@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions genomic sequence that are not annotated as genes but have predic exons by GRAIL are annotated as misc features.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dentified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                         /proteIn_id="AAF04409.1"
/db_xref="G1:6143862"
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/db_xref="G1:6143862"
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SPTRDG1PWATLFGNHUDASFVWPLDWLSSG1PPLKCPAASDDGGCTFRGTTRVEL
IQEDINSGNALSYSM1SPKELWPSVSNVYLDESDBKSFPVALLYFLDSGGSYPEV
ISNAQVEWFKTKSNTLMPYLR1PELIFWHIPSKAYKKVAPRLWITKPCVGSINKEKVV
AQEAENGMMRVLENRSSVKAVFVGHNHGLDWCCPYKDKLWLCFARHTGYGGYGNWPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(877. .929,1009. .1069,1403. .1486,1588. .1644,1737. .1:
1880. .1926,2058. .2148,2480. .2619,2713. .2955,3152. .3230,
3312. .3467,3548. .3744,3890. .3949)
/gene="T22K18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:AAA87568 [Homo sapiens]"
join(<877. 929,1009. 1069,1403. .1486,1588. .1644,
join(<877. 1929,1009. 1069,1403. .1486,1588. .1644,
1737. .1797,1880. .1926,2058. .2148,2480. .2619,2713.
3152. .3230,3312. .3467,3548. .3744,3890. .>3949)
/gene="T22K18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, quality marginal"
complement(437. .495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGRAQVVHDVÝSDPQDSSDSMETPCGDLIFYLDGAHSPESMEACGRWFSSAVRGDKSL
STAILLENCMEVRDPQVLLPKLVTTCASSGTHESRALFVPSMSTVNKVISGASALPSD
TRRKDLTWQFRLQRLMEKSIGGTDAGLDHTLKEDGITALPHDETLGGDAPQCGGPAGT
PVTSSAVMPSLPLTINMLRDCVRRNPSLKLEVLVTGSLHLVGDVLRLLKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MFTSPHLIDVRERFRIDGLDISEEKFLQYFWECWKLLKEKAVDG
LIMPELFQFLIVLAFKLFVCEKFUVAVLEVGLGSTUVIQKEVVCGLASLGNDHM
DILGNTLADIAFKLFVCEKFQOLAFTWVQLGSKADDVLQKTAUNLLEVTIVALAFKLFVKTUDHM
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/note="similar to RecA protein GB:BAA78779
[Rhodopseudomonas palustris]"
complement(join(c46468. 6794,6877. .7016,7118. .7264,7342. .7514,7741. .7828,7938. .8155,8232. .8295,8491.
                                                                                                                                           /note="exon predicted by xgrail, quality good_shadowexon"
complement(<6468. .>8553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (48. .91)
                                                                                                                                                                                                    complement (6053.
                                                                                                                                                                                                                                    SRILEISEMPFRIKTWIRMEDGSVHSEVNLTYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted by genscan+"
join(<4481. .4703,4985. .5477,5564.
/gene="T22X18.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative folylpolyglutamate synthetase"
/protein_id="AAF04408.1"
/db_xref="GI:6143861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="overlap with BAC clone F14P13
(AC009400:87230. .87937)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome="III"
map="CIC5D8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="exon predicted by xgrail, quality marginal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to folylpolyglutamate synthetase"
note="similar to folylpolyglutamate synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="T22K18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="T22K18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(4481. .4703,4985. .5477,5564.
/gene="T22K18.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="T22K18.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             >6035
                                                                                                                                                                                                             .6230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality good_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5732,5817. .6035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5732,5817. .>6035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 2955,
        .>8553))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       С
Е
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                             misc_feature
                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sg
                                                                                                                                           repeat_region
                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLDIALGVGGLPKGRMVEVYGKEASGKTTLALHIIKEAQKLGGYCAYLDAENAMDPSI
ABSIGVNTEELLISRPSSAERMLNIVDLTKSGSVDVIVVDSYAALAPQCELDAPVGE
RYRDTQSRIMTQALRKIHYSVGYSQTLIVELNQVRSHYKSKNMIFPHAEEVTCGGNALP
FHAAIRLKMIRTGLIKTANKYYGLNVCVQVVKNKLAPGKKKSELGIHFGHGFYVEREV
LELACEHGVILREGTSYFIEGEVIEGKDAAEKYLVENKEALDTVVAILRNQLFKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAEYLFGKNTIKEKMEMTTPVVTRKVQSVGEKMEMTTPVITSKAKDQNQWRMSFYMPS
KYGSNLPLPKDPSVKIQQVPRKIVAVVAFSGYVTDEEIERRERELRRALQNDKKFRVR
DGVSEEVAQYNPPFTLPFMRNNEVSLEVENKED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /none="exon predicted by xgrail, quality good_shadowexon" complement (803: .8900) /rpt_family="(TAAA)n" complement (8805: .8840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mmmissssitsslsllssspeklplinpiqrcpitysgfrtasv
NRAIRRQPQSPAVSATESRVSLVLALASQASSVSQRLLADLAMETAKYVFPKRFDSST
NLEEAFMSVPDLETMNFRVLFRTDKYEIRQVEPYFVAETIMPGETGFDSYGASKSFNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="POLY_A"
8974. .9235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(6468. .6744,6877. .7016,7118. .7264,
7342. .7514,7741. .7828,7938. .8155,8232. .8295,8491.
/gene="T22K18.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(10379. .10619,10701. .10790,10871. .10941,11030. .11131,
11228. .11332,11695. .11830,12151. .12260,12341. .12415)
/gene="T22K18.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail, quality
marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (9461. .9610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (8596. .8676)
                             /note="exon predicted by xgrail, complement (14089. .14181)
                                                                                                                                                                                                          complement (13084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (12861. .13364)
/gene="T22K18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted by genscan+, multiple est matches"
complement(12647. .13454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (12526. .12557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAF04411.1"
/db_xref="GI:6143864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted by genscan+, est match"
join(<1979, 10619,10701, 10790,10871, 10941,11030, .1
11228, 11332,11695, .11830,12151, .12260,12341, .>12415)
/gene="T22K18.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASDCELDEVPDDRKVAEKDTALHLALSQLSGDFDKDSKLSLQRFYRKRRVSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MGRLSWASPIQRFRFFSYLSQLNGRRSVLACSGYENRYLSSLVE"
ASDCELDEVPDDRKVAEKDTALHLALSQLSGDFDKDSKLSLQRFYRKRRVSVISTGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="putative_RecA_protein"
/protein_id="AAF04410.1"
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                                                                                                                                                                                                                                                                  TKEKTNGVVRVKMVVSKQELEKLLQGGSVHEMVYRTLAKQHLCDDDDECHKEGWRPLL
                                                                                                                                                                                                                                                                                             /translation="mekkvikimrndgkvveyrgpmkvhhiltqesphyslfdsltnn
ChlhpQakllcgrlyyllpqetnsikhmkkmkkvrpanpevekbeqeedrltdccdn
                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF04412.1"
/db_xref="GI:6143865"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="T22K18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="exon predicted by xgrail, quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="exon predicted by xgrail,
     /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                      note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (12647. .13454)
gene="T22K18.5"
                                                                                                                                                    family="(GAA)n"
ement(17200
                                                                                                                      family="(CAAA)n"
  quality marginal"
                                                              quality good_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality
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REFERENCE
AUTHORS
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AC007475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Dayle, C., Dreenek, D., Farfan, D.,
Perriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Wattei, B., Woshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Saveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Saveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, B., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pieiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                        This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC007475 173613 bp I
Drosophila melanogaster, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 28, 2001 this sequence version replaced gi:6957978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-MAY-1999) Drosophila Genome Center, Laboratory, MS 64-121, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC007475
AC007475.7 GI:13162478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACR04E21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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/clone="BACR04E21 (D592)"
/clone lib="RPCI-98 (Roswell Park Cancer Institute
/crosophila melanogaster BAC library, partial EcoRI
                                                                                          /chromosome="2R"
/map="49A-49B"
                                                                                                                                                                                                              mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                           rain="y; cn bw sp"
xref="taxon:7227"
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
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ORIGIN
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Best Local
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                                                                                                                                                    source
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Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S.,
Phouannavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M., and Venter, J.C.
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BACR14L19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J. M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Pornskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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AC007474.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 28, 2001 this sequence version replaced gi:5670617.
                                                                                                                                                                                                                                                                                            This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location
                                                                                                                                                                                                                                                                                                                                                                                                             Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 192763)
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                                                                                                                                                                                                                                                                                                                                                                                    Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                   This sequence was assembled using end sequences from
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Similarity 90.0%;
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                                                                                                                                                                               Location/Qualifiers
                                 /strain="y; cn bw sp'
/db_xref="taxon:7227"
                                                                                          mol_type="genomic
                                                                                                                   organism="Drosophila"
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Pred. No. 3.5e+02;
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AUTHORS
                                                                                                                           KEYWORDS
SOURCE
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AC109049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                          58864 CTGATGGCCAAACGAGAAAC 58845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE2.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 194634)

Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGATCGCCAAACGAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For more information on this record e-mail to fly@celera.(
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Birect Submission

Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, USA

This sequence was identified as CDM:10212663 by the submitter.

This sequence was identified as CDM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC020286
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                                                                                                                                                                                                                                                                                                                                                            1 CTGATCGCCAAACGAGCAAC 20
                                                                                                                         AC109049
AC109049.4 GI:23101194
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                                                               Rattus norvegicus clone CH230-334A14, ***, 2 unordered pieces.
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Allen,C., Allen,H., Alsbrooks,S., Amin,A., A
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                          Rattus norvegicus
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                                (bases 1 to 206732)
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/Clone="BACR14L19 (D591)"
/Clone= lib="RPCI-98 (Roswell Park Cancer Institute
/Clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6)"
a 41459 c 42141 g 54658 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
42412 c 41301 g 55144 t
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90.0%;
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Pred. No. 3.5e+02;
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er, ***
                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 2; Length 194634;
Pred. No. 3.5e+02;
0; Mismatches 2; Indels 0;
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SEQUENCING IN
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                                                                                                                                                                                                                         SEQUENCING
   ., Adams, C., Alder, J., Anguiano, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly@celera.com.
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G IN PROGRESS
                                                                                            Euteleostomi;
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranike, D., Barber, M., Barnstead, M., Benhmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Besiswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Besiswalo, K., Blair, J., Blankenburg, K., Calvezon, E., Cardenas, V., Carter, K., Cavazoo, I., Ceasar, H., Center, A., Chacko, J., Jacko, J
On Sep 18, 2002 this sequence version replaced gi:21737800. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold, and separated individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 206732)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 206732)
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REFERENCE

AUTHORS TITLE JOURNAL

TITLE JOURNAL

REFERENCE

JOURNAL AUTHORS

COMMENT

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RESULT 14
AC102969
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ORIGIN
                                                                    SOURCE
                                                                                                               VERSION
                                                                                                                                                                            DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                65496
                                                      AC102969.7 GI:30522593
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                      Rattus norvegicus clone CH230-94M19, ***, 5 unordered pieces.
                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                 AC102969
                                                                                                                                                                                                                                                                                                              CTGATCACCAAACCAGCAAC 65515
                                                                                                                                                                                                                                                                                                                                       CTGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: CH230-334A14
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 181594 bases at least Q40
Consensus quality: 184576 bases at least Q30
Consensus quality: 184575 bases at least Q20
Estimated insert size: 197225; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GPTJ
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end_sequence:RXAPN07TJ"
1 40169 c 41232 g 52474 t 18593 others
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6011. .7297
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complement(200587.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10116"
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|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3973: contig of 3973 bp in length 4073: gap of unknown length 206732: contig of 202659 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%;
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Pred. No. 3.5e
0; Mismatches
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3.5e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baldwill, B. Bardarnaike, D. Barberg, M., Barnstead, M., Biswald, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, M. Bhay, C. Burch, P., Burcell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chaper, H., Davis, C., Davy-Carroll, I., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deromo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Degan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagy, M., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, K., Houlins, B., Howells, S., Hulyk, S., Hume, J., Idlabbird, D., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlabbird, D., Jackson, A., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Jackson, L., Li, Z., Liu, J., Liu, W., J., Liu, W., Liu, Y., Londson, B., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kellyy, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Lebow, H., Longacre, S., Marcinez, E., Manshamari, M., Mahindartne, M., Mahmoud, M., Maliby, K., Mangum, A., Manser, G., Minja, E., Montemayor, J., Moore, S., Mooren, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kellyy, S., Kan, Z., King, L., Kovar, C., Karpathy, S., Kellyy, S., Kan, S., Martinaz, E., Mortenayor, J., Moore, S., Moore, S., Mortis, S., Munidasa, M., Murphy, M., Nair, L., Martinaz, E., Montenayor, J., Martinaz, E., Montenayor, J., Kelly, R., Moore, S., Reyes, K., Regier, M., Reigh, R., Plazo, M., Store, J., Scorelle, R., Sosa, J., Shen, H., Store, J., Shen, H., Store, R., Kell
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819627.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 255345), Marie, Muzny, D. Marie, Meter, M.Lee., Abramzon, S., Adams, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D. Allen, H., Alsbrooks, S., Amin, A., Anguiano, D. Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, Anyalebechi, V., Aoyagi, A., Barber, M., Barnstead, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
3 (bases 1 to 259345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Direct Submission
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 259345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams, C., Alder, J.,
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FEATURES
                                                                       RESULT -15
AC103330
                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                           DEFINITION
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                  204951 CTGATCACCAAACCAGCAAC 204970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole gen shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 table.
                     AC103330 261157 bp DNA linear HTG 13-MAY-2003. Rattus norvegicus clone CH230-177K18, WORKING DRAFT SEQUENCE, 7
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                      CTGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                        79986
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Center clone name: CH230-94M19

Center clone name: CH230-94M19

Center clone name: CH230-94M19

Center clone name: CH230-94M19

Center clone name: Atlae 3.0;

Assembly program: Atlae 3.0;

Consensus quality: 242269 bases at least Q40

Consensus quality: 247151 bases at least Q30

Consensus quality: 24910 bases at least Q20

Estimated insert size: 260613; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248467
248567
254508
254608
256456
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                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_end_extension
clone_end:T7"
1 53670 c 51512 g 6682'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end_sequence:BH355461"
251214. .254507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_contig"
complement (245699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="CH230-94M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 25934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248466: contig of 248466 bp in length 248566: gap of unknown length 254507: contig of 5941 bp in length 254607: gap of unknown length 256455: contig of 1848 bp in length 256555: gap of unknown length 256555: gap of unknown length 256556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Genome Center
                                                                                                                                                                                                                                                                                                                84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58260: gap of unknown 59345: contig of 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                        51512 g 66827 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 1605 bp in length
gap of unknown length
contig of 1085 bp in length
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 2;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                              7350 others
                                                                                                                                                                                                                                                                                                                                              Length 259345;
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REFERENCE
AUTHORS
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                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
REFERENCE
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                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anyalebecni, V., Aoyedi, M., Ayodej, M., Baldwin, D., Bandaraniake, D., Barber, M., Barnstead, M., Broam, M.,
Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, M., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Cessar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, C., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Dalyada, O., Denson, S., Dersmo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerer, M., Goster, M.,
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerer, M., Goster, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerer, M., Goster, M., Guerer, M., Marlin, M., J., London, P., Johnson, R., Johns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D. Allen, C., Allen, H., Ayodeji, M., Baca, E., Baden, Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC103330 GI:30580846
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:22857506.
                                                                                                                                                                                                                                                                              Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                          of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 261157)
                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Niederhausern, A., Weiss, R., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                     Rat Genome Sequencing Consortium.
                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 261157)
                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 261157)
                                                                                                                                                                                                                                                 TX 77030,
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Gaps

<u>.</u>

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BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
Query Match
Best Local Similarity
                                                                                                                                                            misc_feature
                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
                                                                                                               66925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Atlas 3.0;
Consensus quality: 247708 bases at least Q40
Consensus quality: 250022 bases at least Q30
Consensus quality: 251823 bases at least Q20
Estimated insert size: 259364; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242049
242149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CH230-177K18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GLAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246132
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                                                                                                                                                                                                                                                                                                                              5033.
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/clone="CH230-177K18"
                                                                                                       /note="wgs_contig"
60485 c 60256 g
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242149. .243506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                        'note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                         2340
     90.0%;
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242148: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 3983 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
     Score 16.8; DB 2;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g of 1056 bp in length
if unknown length
g of 2087 bp in length
if unknown length
g of 1905 bp in length
if unknown length
g of 3369 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 6109 bp in length unknown length
                                                                                                             65490 t
                                                                                                             8001 others
                         Length 261157;
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Search completed: February 12, 2004, 04:41:47 Job time: 591.854 secs

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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2552756 seqs, 1349719017 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-692-077D-15
20
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(without alignments)
SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

(SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

(SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

(SIDS1/gcgdata/geneseq/geneseqn-emb1/NA199).DAT:*

(SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

(SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*

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(SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*

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_/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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15.8	15.8	15.8	15.8	15.8	16.8	16.8	. 20	Score
79.0	79.0	79.0	79.0	79.0	84.0	84.0	100.0	Query
108213	47999	5786	1976	277	6990	3920	100.0 20 2	Query Match Length DB
3 21	25	22	25	25	23	23	23	BG
	AAD52898	AAS29976	ABX22622	ABX25006	ABL22104	ABL22105	AAI99909	Query Match Length DB ID
Arabidopsis thalia	Human tweety homol	Human lung antigen	Human GDP-mannose	Human GDP-mannose	Drosophila melanog	Drosophila melanog	Human alpha-2BAR g	Description

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304 391	180	5379					on	8189	7874	6080	4779	3907	3281	3266	2888	2193	2036	1588	1586	1525	1525	1525	1525	1380	1359	1359	1284	1281	705	309	144	536165	534720	543
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ABX51029	AAQ49414	ABL06846	AB100340	AAS86718	ABL06847	AAS94178	AAV21209	ABL01888	AAX20568	ABL01846	AAS29952	ABL14338	ABT17861	ABL01889	ABL02530	AAS53007	ABL01847	AAC41102	AAC45525	ABQ45083	ABQ45082	ABQ44153	ABQ44152	ABL14339	ABZ14216	ABZ66820	ABT19049	ABT18455	ABQ65658	ABQ91594	ABQ91593	AAV30459	AAV30458	ABN68569
Human secreted pro Bovine EST associa	Cytochrome P450 ho	Drosophila melanog	DNA encoding novel	DNA encoding novel	Drosophila melanog	DNA encoding novel	Methanococcus jann	Drosophila melanog	Polynucleotide seq	Drosophila melanog		Drosophila melanog	Aspergillus fumiga	Drosophila melanog	Drosophila melanog	_	Drosophila melanog	Arabidopsis thalia	Arabidopsis thalia	Oligonucleotide fo				melan	Arabidopsis thalia					_	M. capsulatus gene	Rhizobium species	Rhizobium species	Streptococcus poly

ALIGNMENTS

AAI99909 standard; DNA; 20

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RESULT 1
AA1999
ID AA199
ID AA199
XX AA19
XX AA19
XX Huma
XX Huma
XX Huma
XX Phomo
OS Homo
OS Homo
OS 17-A
XX 11-A
XX 11-A
XX 25-O
XX 25-O
XX 11-A
XX 11-A
XX 13-C
XX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss.
                                                                                                                                                                                                                                                17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alpha-2BAR genotyping PCR primer SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002 (first entry)
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Liggett SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-2001; 2001WO-US12575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200179561-A2.
                                                                                                (LIGG/) LIGGETT S B.
(SMAL/) SMALL K M.
     Small KM;
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ABL22105
ID ABL2
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AC ABL2
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PR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC (b) detecting a polymorphic site comprising nucleotide positions 901-909 CC of (I), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (999999999999) or (B) (9999999529) at CC positions 961-972 of (III). The method may be used for genotyping an CC whether an individual is at increased risk of developing a disease CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. polimbine, prazosin, ARC 239, CC combinations of these) antagonist (e.g. yohimbine, prazosin, ARC 239, CC combinations, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC levels). The present sequence is that of a human alpha-ZBAR PCR primer, we seem to the sequence of the invention.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL22105
                                                                                          (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL22105 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 7 A; 7 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I) a site comprising cytosine or guanine at position 753 of (IIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease associated with the a polymorphic site -
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                                                                                       CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster genomic polynucleotide SEQ ID NO 17788.
                                                                                                                                                                                                                                                                                                                                                                                                   melanogaster
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                           Adams M,
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                                                                                                                                        2000US-191637P.
2000US-0614150.
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                           PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                           Myers
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Best Local S
Matches 18
                                                              Claim 1; SEQ ID NO 17785; 21pp + Sequence Listing;
                                                                                               New isolated nucleic acid
genes from Drosophila and
                                                                                                                                WPI;
                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 17785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryones for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proresised DNA (ABB57737-ABB72072)
                                                                                        interactions
                                                                                                                                                   Venter
                                                                                                                                                                                                                    23-MAR-2001;
                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                            WC200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                       ABL22104;
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                                                                                                                                                                                                                                                                                                                                                                                                     104/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3920 BP; 1053 A; 1007 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the specification, but was obtained in electronic format direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                            .3432
                                                                                                                            2001-656860/75.
                                                                                                                                                 JC,
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                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                           developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                    2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                  gene;
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                                                                                                                                              PWD,
                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                       biology; cell signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.8;
Pred. No. 5
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                                                                                                                                              EW;
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                                                                                                                                                                                                                                                                                                         insecticide;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

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RESULT 4
ABX25006/c
ID ABX25006 standard; cDNA; 277 BP
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AC ABX25006;
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DT 11-FEB-2003' (first entry)
DE 11-JUN-2001; 2001US-0878574.
DT 11-JUN-2001; 2001US-0878574.
DT 22-NOV-1996; 96US-0753233.
DT 22-NOV-1996; 96
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      4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the level of cellular fucosylation or diseases include arthritis, transplant rejection, asthma, sepsis, repertusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for soreening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences (ABL0184)
(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) tide, for manufacturing complex carbohydrates, or as targets for ening GM4,6D antagonists for treating e.g. arthritis, or transplant
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Pred. No. 60;
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format directly from WIPO
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                The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polymucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polymucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide, for screening
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                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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                      26-JUL-2000
26-JUL-2000
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04-FEB-2000

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02-MAR-2000

16-MAR-2000

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07-JUN-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; cerebrovascular disorder; breast; liver; cardiovascular disorder; ds; fungal infection; viral infection; ocular disorder; bacterial infection; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
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08.DEC-2000
Alzheimer's disease, infections caused by bacteria, virtues and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                     Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode the lung antigen polypeptides of the invention. Lung antigen polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as cardiac arrest, cerebrovascular such as
                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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2000US-0249265.

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2000US-0251030.

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Query Match

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Score 15.8;

DB 22;

Length 5786;

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RESULT 8
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Best Local S
Matches 17
                                                                                                                                                                           The invention relates to human tweety homologue 2 (TTYH2) polypeptide and polynucleotide sequence. TTYH2 is useful for producing an antigen-binding molecule that is immuno-interactive with the polypeptide. The agent is useful for manufacturing a medicament for restoring a normal level and/or functional activity of TTYH2 expression in a patient, and for treating or preventing cancer or tumour. TTYH2 sequences may also be used to provide both drug cargets and regulators to promote or inhibit one or more activities, and to provide diagnostic markers for cancers. The present sequence is human TTYH2 gene.
                  20-MAR-2001
                                    AAF22305;
                                                   AAF22305 standard;
                                                                                                                                                             Sequence 47999 BP; 11178 A; 12727 C; 12874 G; 11209 T; 11 other;
                                                                                                                                                                                                                                                                   Claim 10; Page 128-156; 176pp;
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89.5%;
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Pred. No. 2.3e+02;
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27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
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18-MAY-1999;
13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN68569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 68; Page 977-1388; 1449pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana chromosome 4 centromere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCH-) UNIV
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Similarity 89.5%;
17; Conservative
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99US-0153584.
99US-0154603.
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Pred. No. 2.8e+02;
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RESULT 10
AAV30458/c
D AAV30458 standard; DNA; 534720 BP
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acide encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
     Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-352536/38.
P-PSDB; ABP27938.
                                                                                                                                                                                Rhizobium ep
                                                                                                                                                                                                                      Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
                                                                                                                                                                                                                                                                                            14-OCT-1998
                                                                                                                                                                                                                                                                                                                       AAV30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 543 BP; 123 A; 90 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 3667; 4525pp; English.
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Tettelin H;
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INST GENOMIC RES
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                                                                                                                                                                                                                                                                species plasmid pNGR234a.
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                                                                                                                                                                                                                                                                                            (first entry)
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                                                                    /standard_name= "ORF K1"
/product= "oligopeptide permease"
/note= "homologous to the OppC ges
418673..419680
                                                                                                                                        Location/Qualifiers
417796..418671
            '*tag= b
/standard_name= "ORF K2"
/product= "oligopeptide permease"
/note= "homologous to the OppD ger
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Pred. No. 2.6e+02;
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/*tag= q
/standard name= "
/gene= "fixC"
/product= "protei
                                                                                                                                                                                                        /product= "protein involved
biosynthesis"
complement (436460..438130)
                                                                                                                                                                                                                                                                                        /standard_name= "ORF K13"
/product= "ferrodoxin/ferrodoxin-like protein"
/note= "homologous to the FdxN gene"
complement (434753..436234)
                                                                                                                                                                                                                                                                                                                                                                                                               /product="mprotein of unknown function" /note= "homologous to the FixU gene" complement (434107..434433)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ystandard_name= "ORF K10"
/product= "transposase homologue"
/note= "homologues to the Inp gene
complement (433880..434110)
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/product= "transposase homologue"
/complement (431296..432840)
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/product= "glutamate dehydrogenase-like protein"
/note= "homologous to the GLUD1 gene"
complement (430538..431284)
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/product= "(semi)aldehyde dehydrogenase-like protein"
complement (426949..428028)
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/standard name= "ORF K3"
/product= "oligopeptide permease"
/note= "homologous to the OppF ges
/20774...422159
                                                      /product= "protein required
complement (438605..439912)
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/standard_name= "ORF K5"
/product="aminotransferase-like protein"
/product="aminotransferase-like protein"
                                                                                                                          complement (438297..438590)
                                                                                                                                                                                                                                                                                                                                                              /product="protein of unknown
complement (434517..434711)
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/product= "transposase homologue"
/note= "homologous to the Tnp gen
                                                                                                                                                                  /standard_name
/gene= "nlfA"
                                                                                                                                                                                                                                                 gene= "nīfB"
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/product= "encapsulation-like protein"
/note= "homologous to the CapA gene"
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                                                                                  gene= "fīxX"
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                                                                                                _name= "ORF K16"
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                                                                                                                                                                                                                                                                 name= "ORF K14"
  "protein required for nitrogenase activity"
                                                                                                                                                     "positive regulator
                               "ORF K17"
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                                                                    for nitrogenase activity"
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                         /note= "homologous to the FixF gene" 459093..459575
                                                        457687..459096
                                                                                                                                        /standard_name= "ORF L8"
/product= "protein involved in
biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
/note= "homologous to the Lina 448497..450203
                                                                                                                                                                                                 /product= "beta-subunit
156187..457677
                                                                                                                                                                                                                                 standard_name= "ORF L7"
gene= "nifk"
                                                                                                                                                                                                                                                                       /product= "alpha-subunit of 454590..456131
                                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF L4"
/product= "luciferase alpha-subunit-like protein"
/pote= "homologous to the LuxA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447844 . . 448500
                                                                                                                                                                                                                                                                                                                   standard_name=
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/product= "gamma-hexachlorocyclohexane-dechlorinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF L1"
/product= "cytochrome P450-like protein"
/note= "homologous to the CamC gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name= "ORF K20
/product= "protein of unknown
complement (443313...443879)
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complement (442316..442636)
                                                                                                                                                                                                                                                                                                       gene= "nifD"
                                                                                                                                                                                                                                                                                                                                                                                                                             standard_name= "ORF L3"
product= "putative protein with degradative function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "protein required complement (441042..441899)
                                                                                                                                                                                                                                                                                                                                                                                                                    50341..451396
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46599..447843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "C4-dicarboxylate transport protein" note= "homologous to the DctAI gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'etandard name= "ORF K22"

'product= "ferrodoxin-like protein"

'note= "homologous to the NifQ gene"

145088..446602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard_name= "ORF K21"

product= "protein of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_nam
/gene= "flxB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (439923..441032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene= "fīxA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard
                                                                                                                            "homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _name= "ORF K19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _name= "ORF K18"
                                                                                                                                                                                                                                                                                                                   "ORF L6"
                                                                                                                                                                                                                  õ,
                                                                                                                            NifB gene'
                                                                                                                                                                                                                 FeMo
                                                                                                                                                                                                                                                                                      FeMo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                        FeMo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function'
                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitrogenase activity
                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitrogenase activity"
                                                                                                                                                        co-factor
                                                                                                                                                                                                               0f
                                                                                                                                                                                                                                                                                   of nitrogenase"
                                                                                                                                                                                                               nitrogenase'
      RESULT 11
AAV30459/c
ID AAV304
XX AAV304
XX Symbio
DE Rhizob
XX Symbio
CKW degrad
KW 1egume
XX U09802
XX W09802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
New isolated symbiotic plasmid from Rhizobium sp. NGR234 -develop products for modifying plant characteristics, e.g. fixation, synthesis of compounds and stress response
                                                              WPI; 1998-110606/10
                                                                                                                      (MOLE-)
                                                                                            Broughton
                                                                                                                                                                20-MAY-1997;
12-JUL-1996;
                                                                                                                                                                                                         10-JUL-1997;
                                                                                                                                                                                                                                      22-JAN-1998.
                                                                                                                                                                                                                                                                   WO9802560-A2
                                                                                                                                                                                                                                                                                            Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV30459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV30459 standard; DNA; 536165
                                                                                                                                                                                                                                                                                                                        legume; plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433213
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                                                                                                                      INST MOLECULAR BIOTECHNOLOGY.

LAB BIOLOGIE MOLECULAIRE PLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATCGCCAATCGAGCA 433197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATCGCCAAACGAGCA 18
                                                                                                                                                                                                                                                                                            ds.
                                                                                                                                                                                                                                                                                                                                                                              species symbiotic plasmid pNGR234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                       Freiberg CB,
                                                                                                                                                               97GB-0010395.
96EP-0730001.
                                                                                                                                                                                                       97WO-IB00950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "ORF L12"
/product= "protein similar to p
/product= "protein similar to p
of nitrogenase"
/note= "homologous to the NifH
461228..461545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464736..466079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard_name= "ORF L14"
(product= "peptidase-like
)note= "homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459579..460067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF L10"
/product= "protein of unknown function"
/note= "homologous to the NifX gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product= "protein of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60501..460920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.0%;
94.1%;
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                                                                                       Perret XP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
                                     BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "ORF L15"
/product= "processing protease-like protein"
/note= "homologous to the PP gene"
466590..467021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name= "ORF L13"
/product= "protein of unknown function'
43201..464739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4; DB 19;
Pred. No. 4.3e+02;
0; Mismatches 1;
 Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein"
bl:MPP gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene"
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A,
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e.g. nitroger

used to

Claim 1;

Fig

3; 228pp;

the nucleotide

веquence English

of the plasmid pNGR234a isolated from

Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the nucleotide sequences or ORFs can be used e.g. in the transportation of compounds to and from an organism which is a host to at least one of the nucleotide sequences, ORFs or proteins, the degradation and/or metabolism of organic, inorganic, natural or xenobiotic substances in a host organism or the modification of the host range, nitrogen fixation abilities; for obtaining a synthetic minimal set of ORFs required for functional Rhizobium-legume symbiosis,

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M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the invention.
                                                                 The invention relates to a novel DNA array giving a representation of number of Methylococcus capsulatus genes. The method of the invention useful for determination of the differential expression of the genes c
                                                                                                                                                   Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                     Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                               14-JAN-2002; 2002WO-NO00019
                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002
                                                                                                                                         capsulatus
                                                                                                                                                                                                   WPI; 2002-557818/59
                                                                                                                                                                                                                                                                                                                                                                                              WO200255655-A2
                                                                                                                                                                                                                                                                          (UNIF-) UNIFOB (TIGR-) TIGR.
                                                                                                                                                                                                                                                                                                            12-JAN-2001;
12-JAN-2001;
                                                                                                                                        genes
                                                                                                                                                                                                                                                                                                            2001NO-0000235.
2001NO-0000239.
                                                                                                                                                                                                                                                                                     STIFTELSEN UNIV BERGEN
                                                                                                                                                                                                                                     Eidhammer I,
Lossius I,
                                                                                                                 678pp; English.
                                                                                                                                                                                                                                      Eisen JA,
                                                                                                                                                                                                                                                Jonassen
                                                                                                                                                                                                                                      Fraser
                                                                                                                                                                                                                                     Jensen HB, Lien T
ser CM, Durkin AS;
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Sequence 144 BP; 30

Α,

50

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0 other;

RESULT 14
ABQ65658/c
ID ABQ656
XX
AC ABQ656

ABQ65658

standard; DNA; 705

ΒP

ABQ65658;

19 B

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RESULT 13
ABG91594/c
ID ABG915
XX ABG915
XX O1-OCT
XX Micro
DT O1-OCT
XX Micro
OS Methy]
XX Wicro
OS Methy]
XX I2-JA
PR 12-JA
PR 
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                                                                                                                                Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                  M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for weak in the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel DNA array giving a representation of number of Methylococcus capsulatus genes. The method of the invention useful for determination of the differential expression of the genes of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABQ91594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABQ91594 standard; DNA; 309 BP
                                                                                                                                                                                                                                                                        Sequence 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capsulatus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylococcus capsulatus genes, oligonucleotides representative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-557818/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salzberg SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lillehaug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birkeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-2001; 2001NO-0000235
12-JAN-2001; 2001NO-0000239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2002; 2002WO-NO00019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylococcus capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micro array; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIF-) UNIFOB (TIGR-) TIGR.
   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                    l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
   CTGATCGCCATACGGGCGAC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGATCGCCATACGGGCGAC
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                                                                   CTGATCGCCAAACGAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                        B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene #1579 for DNA array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STIFTELSEN UNIV BERGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eidhammer I, Jonassen
Lossius I, Eisen JA,
                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; differential expression; gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678pp;
                                                                                                                                                                                                                                                                        A; 86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%;
85.0%;
                                                                                                                                                                    76.0%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                    0,
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Pred. No. 2.
                                                                                                                                                                        Score 15.2;
Pred. No. 3.
                                                                                                                                                                                                                                                                        109 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
                                                                   20
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                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I, Jen
Fraser
                                                                                                                                                                                                                                                                            Η,
                                                                                                                                                                        .1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jensen
ser CM,
                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멂
                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HB, Lie
Durkin
                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                           309;
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RESULT 12 ABQ91593

ABQ91593;

ABQ91593 standard;

DNA;

144

ВP

M. capsulatus

gene (first

#1578 for DNA array.

entry)

Methylococcus Micro array; gene;

capsulatus.

ds;

differential expression; gene expression.

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433213

TGATCGCCAATCGAGCA 433197 TGATCGCCAAACGAGCA

18

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Query Match Best Local S Matches 16

Similarity

77.0**%**; 94.1**%**;

16;

Conservative

0

Score 15.4; D Pred. No. 4.3e 0; Mismatches

.3e+02

DB 19;

Length

536165; 0

Indels

Gaps

0

111255 T; 0 other;

Sequence 536165 BP; 111291 A; 155755 C; 157864 G; especially for nodulation efficiency on host plants.

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Arabidopsis thaliana; thale cress; stress; metabolic pathway; biosynthinsecticide; antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2002
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                                                    Query Match
Best Local S
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                                          Matches
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Rameaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LEDF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MATH/)
                                                                                                                                                          The invention relates to nucleic acids (1) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or produce genetically modified plant cells or transgenic plants, which to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered may have improved resistance to disease or stress, or altered, netabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents (e.g. fungicides, or can be used to screen for biologically active agents).
                                                                                                                                                                                                                                                                                                                             New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistan or altered metabolism
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-479224/51.
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                                                                                                                                                                                                                                                                                                                                                                                                               Hurban P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRIC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GARC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HAAS/)
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 235; 40pp + Sequence Listing; English.
                                                                                             Sequence
                                                                                                                           OIGSD
                                                                                                                                       specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMILTON C M.
PRICE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GORLACH J.
                                                                                                                      The sequence data for this patent did not form part of the fication, but was obtained in electronic format directly fro at seqdata uspto.gov/sequence.html?DocID=999909770149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAINES T M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAAS W D.
GARCIA C A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOESSNER J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HURBAN P.
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                                                         Similarity
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, Page A, M
, Kricker M,
CTGATCGCCAAACGAGCAAC
                                                                                                 705 BP; 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamilton CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mathew AV,
M, Slater T,
                                                                                                    A; 135
                                                             76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e cress; plant; transgenic; GMO; disease; biosynthetic pathway; nutrition; fungicide;
                                                                                                       C; 183 G;
                                                   0
                                                               Score 15.2; DB 2
Pred. No. 3.4e+02
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Ledford BL,
, Davis KR,
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                                                    Mismatches
                                                                                                            200
                                                                                                          T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raines TM,
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                                                                                  24;
                                                                                  Length
                                                          Indels
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; JP, Haas WD;
Hoffman N;
                                                                                        705;
                                                                                                                                                                                                                                                                                                                                                                  resistance
                                                               0
                                                               Gaps
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δ

Query Match

Sequence 1281 BP;

300 A; 358

C; 333 Score

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15.2; G

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25;

Length 1281;

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                                                                                                        CC essential genes of Aspergillus fundgatus. The isolated nucleic acids of cc essential genes of Aspergillus fundgatus. The isolated nucleic acids of cc the invention are used to treat or prevent infections by a pathogenic cc subject (e.g. cancer), to prevent or contain contamination of an object (co subject (e.g. cancer), to prevent or inhibit formation on a surface of a cc by A. fundgatus, or to prevent or inhibit formation on a surface of a by A. fundgatus. The polynucleotides are useful for characterisation, screening or comparising A. fundgatus. The polynucleotides are useful for characterisation contamination of an object comparism invade or reside, for comparing with the pathogenic corganisms invade or reside, for comparing with the pathogenic organisms invade or reside for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A.

CC fundgatus to identify duplicated genes or paralogues having the same or comparisms invade or related or distant pathogenic organisms to identify similar biochemical activity and/or function, for comparing with DNA comparing of other related or distant pathogenic organisms to identify and sequences of other related or distant pathogenic organisms to identify and sequences of other related or distant pathogenic organisms to identify and or expense, and for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an comparing or to identify inhibitors of the binding contracterion. The polypeptides may be used to raise antibodies or to bick the protein of the protein in assays designed to quantitatively the transe in which bathogenic organism invade or reside, and to determine levels of the protein in assays designed to anarker for determine in which bathogenic organism invade or reside, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001; 2001US-285697P.
27-APR-2001; 2001US-287066P.
25-JUN-2001; 2001US-25890P.
09-JUL-2001; 2001US-303899P.
31-AUG-2001; 2001US-316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABT18455 standard; DNA; 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200286090-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2002; 2002WO-US13142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-093124/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections A. fumigatus, or for treating a non-infectious disease in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page -; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. cancer
                                 host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essentigenes of Aspergillus fumigatus of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de; cytostatic; essential gene; Aspergillus fumigatus; infection; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCATCGCCAGACGAGCACC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fumigatus
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                         290
                           T; 0 other;
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                                                                                         essential
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Issued_Patents_NA:*
1: /cgn2_6/pcodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/pcodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match Length
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                                                            774.0
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3032
536165
36470
1664976
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543
                      GenCore version 5.1.6 (c) 1993 - 2004 Compugen
   4 US-09-328-35-643
4 US-09-221-017B-347
4 US-09-214-808-1
4 US-08-311-731A-123
5 4 US-08-916-421B-1
1 US-07-912-900-25
1 US-08-285-309-25
2 US-08-285-309-25
2 US-08-107-532A-2028
1 US-09-107-532A-2028
1 US-09-107-532A-2028
1 US-09-103-840A-1
3 US-09-103-840A-2
3 US-09-103-840A-2
3 US-09-103-840A-2
3 US-09-103-840A-1
4 US-09-483-597-218
4 US-09-483-597-218
4 US-09-483-597-60
1 US-09-684-21B-60
1 US-09-684-21B-60
1 US-09-689-751-108
US-09-689-751-108
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Sequence 643, App
Sequence 147, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 25, Appl
Sequence 25, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 218, Appl
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Sequence 218, Appl
Sequence 218, Appl
Sequence 60, Appl
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US-09-328-352-643/c
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29 14.2 71.0 814 4 US-09-439-313-36 30 14.2 71.0 814 4 US-09-352-616A-36 31 14.2 71.0 814 4 US-09-232-149A-36 32 14.2 71.0 816 4 US-09-221-017B-199 33 14.2 71.0 1185 4 US-09-221-017B-199 34 14.2 71.0 1185 2 US-09-96-685-13 35 14.2 71.0 1194 2 US-09-96-685-13 36 14.2 71.0 1194 3 US-08-996-685-13 37 14.2 71.0 1428 4 US-09-107-532A-858 38 14.2 71.0 1428 4 US-09-107-532A-858 39 14.2 71.0 1597 2 US-08-989-478-9 39 14.2 71.0 1597 3 US-08-98-685-9 40 14.2 71.0 1597 3 US-08-996-685-11 41 14.2 71.0 1608 3 US-08-996-685-11 42 14.2 71.0 2011 2 US-08-999-478-6 43 14.2 71.0 2011 3 US-08-999-478-6 44 14.2 71.0 2011 3 US-08-996-685-6 45 14.2 71.0 2011 3 US-08-996-685-7
2 71.0 814 4 2 71.0 814 4 2 71.0 816 4 2 71.0 1185 4 2 71.0 1194 3 2 71.0 1428 4 2 71.0 1597 3 2 71.0 1597 3 2 71.0 1608 3 2 71.0 2011 2 2 71.0 2011 3
.0 814 4 .0 814 4 .0 814 4 .0 814 4 .0 1185 4 .0 1194 2 .0 1194 2 .0 1199 3 .0 11597 2 .0 1597 3 .0 1608 2 .0 1608 2 .0 2011 2 .0 2011 3

US-09-439-313-36 US-09-352-616A-36 US-09-252-149A-36 US-09-252-149A-36 US-09-252-91A-1931 US-08-96-685-13 US-08-996-685-13 US-08-996-685-9 US-08-98-478-11 US-08-98-478-11 US-08-98-478-11 US-08-98-478-11 US-08-98-478-685-11 US-08-98-478-7

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 643
LENGTH: 1698
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-643
                                                                                                                                                                                                                                                                                                                                                                                      US-09-221-017B-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 643, Application Patent No. 6562958
COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                               Sequence 347, Applicat Patent No. 6444799
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            APPLICANT: ROSS, Bru
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                          STREET: 755 PAGI
                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
                                                                                                                                                                                                                                                                                                                                                   347, Application US/09221017B
o. 6444799
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N: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
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94.1%;
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Pred. No. 44
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APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT: INFORMATION:

PCT/AU98/01023

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 30-JA

30-JAN-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-DEC-

PP1182

INFORMATION FOR SEQ ID NO:

TELEPHONE:

650-494-0792

650-813-5600

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER:

27340-20021.00

NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430

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; SEQ ID NO 1
; LENGTH: 536165
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1
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                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-214-808-1/c
                                                                                                                                                                                                                                                  APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Kavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793
TITLE OF INVENTION: Plasmid
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09214808A
Patent No. 6475793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/214,808/
CURRENT FILING DATE: 1999-06-22
                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NAMII-SENSE: UNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3032 base pairs
TYPE: nucleic acid
STRANDENESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 1...3032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2855 CTGATCGCCATACGAGC 2871
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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Similarity 94.1%;
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                                                                                                                                    Ver. 2.1
77.0%;
94.1%;
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Pred. No. 4
Score 15.4;
Pred. No. 80;
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US-08-916-421B-1/c

Sequence 1, Application US/08916421B Patent No. 6503729

GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc
Patent No. 6503729
TITLE OF INVENTION: Jannaschii

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RESULT 5
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                                                                                                               Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                            ORIGINAL SOURCE: ORGANISM: MYC
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SMITH,
APPLICANT: MAO, J
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617/720-3500
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                                               3894 CTAATCGCCACACAAGCAAC 3913
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                                                                                                                              Similarity
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                                                                           CTGATCGCCAAACGAGCAAC 20
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                                                                                                             Conservative
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85.0%;
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                                                                                                           o
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                                                                                                           Score 15.2; [Pred. No. 79; 0; Mismatches
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                                                                                                                                           Length 36470;
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CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOPTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (163385) .(163385)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (191989) .(191989)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (191995) .(191995)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (231980). (231980)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (234187). (234187)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (234220). (234220)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (234220). (234220)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (234814). (234814)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (309398). (309398)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (103998) . (103998) OTHER INFORMATION: n equals a, t NAME/KEY: misc feature LOCATION: (148948) . (148948) OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (2825). (28258) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (84773). (84773)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals
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LOCATION: (98120) ... (98120)
OTHER INFORMATION: n equals
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
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OTHER INFORMATION: n equals
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LOCATION: (98343)..(98343)
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NAME/KEY: misc reacure LOCATION: (1349473)(134947 OTHER INFORMATION: n equals	YALI: misc reacure TION: (1313224)(131322 R INFORMATION: n equals	YEY: misc reacure (1310988)(131098 R INFORMATION: n equals	YEEK: misc reduire TION: (1130881)(113088 R INFORMATION: n equals	TION: (111988)(111988 R INFORMATION: n equals	TION: (1096846)(109684 R INFORMATION: n equals	TION: (1084830)(108483) R INFORMATION: n equals	INFORMATION: n equals	TON: (855539)(855539) INFORMATION: n equals	ION: (779676)(779676) INFORMATION: n equals	YKEY: misc reacure TION: (779455)(779455) R INFORMATION: n equals	YALY: misc reacure TION: (741684). (741684) R INFORMATION: n equals	TION: (713652). (713652) R INFORMATION: n equals	TION: (682442)(682442) R INFORMATION: n equals	N: (674435) . (674435) NFORMATION: n equals	TION: (657203)(657203) R INFORMATION: n equals	TION: (657081). (657081) R INFORMATION: n equals /KRY: misc feature	TION: (622708) R INFORMATION: n equals /KEY: misc feature	(600992)(600992) ORMATION: n equals	TION: (559241)(559241) R INFORMATION: n equals	: (559167)(559167) FORMATION: n equals	TION: (319226)(319226) R INFORMATION: n equals	YEY: misc reducte (312993)(312993) R INFORMATION: n equals	TION: (312837)(312837) R INFORMATION: n equals	NAME/KEY: misc feature
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US-07-912-900-25
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Patent No. 53491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, v
CURRENT APPLICATION DATA:

APPLICATION UMBER: US/07/912,900
FILING DATE: 1920713

CLASSIFICATION: 800
                                         TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1637998)...(1637998)
OTHER INFORMATION: n equals a,
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LOCATION: (1664854)..(1664855)
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LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a,
                            SEQUENCE CHARACTERISTICS:
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1603734)...(1603734)
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID FITTLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
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                                                                       TELEFAX:
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                                                                                      TELEPHONE:
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              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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1 Similarity 85.0%;
17; Conservation
                                                                                                                                                                                                                                                                                                                       11530
                                                                                                                                                                                                                                                                                                                                                Garden City
: New York
: 543 base pairs
NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                               E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
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                                                                       (516) 742-4366
                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lester, Diane R.
                                                                                       (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feature
                                                                                                                                                                                                                                         Release #1.0, Version #1.25
                                                                                                                                                                                                            US/07/912,900
                                           25:
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Pred. No. 9
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; MOLECULE TYPE:
US-08-285-309-25
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-912-900-25
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                                                          Matches
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Tocal Similarity
                                                                                                                                                                                                               TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tanaka, yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
TITLE OF INVENTION: HYDROXYLASE AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 03-AUG CLASSIFICATION: 800
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STATE: New York
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69 TGATCGCCAAACTATCAA 86
                                                         16;
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                          2 TGATCGCCAAACGAGCAA 19
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                                                                                                                                                                            nucleic acid
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400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08285309
                                                         Conservative
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                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1994
                                                                                                                                                            single
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88.9%;
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88.9%;
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                                                                       Score 14.8;
Pred. No. 8
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Pred. No. 80;
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                                                                                   DB 1;
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                                                                                  Length 543;
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                                                       Indels
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RESULT 8 US-08-502-046-25 VS-08-502-046-25, Application US/08502046 Sequence 25, Application US/08502046 Patent No. 5861487 0

GENERAL INFORMATION:

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RESULT 9
US-08-313-075A-31
; Sequence 31, Application US/08313075A
; Patent No. 5639870
; Patent Tonnamion:
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COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-JUL-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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TELEFAX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
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FILING DATE: 03-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,34
REFERENCE/DOCKET NUMBER: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
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MOLECULE TYPE:
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APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,
TITLE OF INVENTION: HYDROXYLASE AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
                                                                                                                            APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          APPLICANT: Holton, Timothy A. APPLICANT: Cornish, Edwins C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
OMPUTER READABLE FORM:
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STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                    COUNTRY: U
                                                                      ADDRESSEE: Scully, Scott, Mur
STREET: 400 Garden City Plaza
CITY: Garden City
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                                                      New York
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                                  U.S.A.
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                                                                                                            Murphy & Presser
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                                                                                                                                                                                                                                                                                                                             Sequence 2006 6583275
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A NUCLEIC ACID
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2028, Application US/09107532A
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-JAN-1993 PRIOR APPLICATION DATA:
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: AU P. FILING DATE: 27-MAR-1992
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COMPUTER: IF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 547 base pairs
                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGATCGCCAAACGAGCAA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                      COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998
                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                      ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..514
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                       100 Beaver Street
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Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                     and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 547;
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NAME/KEY: misc feature LOCATION: (B) LOCATION 1...810 SEQUENCE DESCRIPTION: SEQ ID NO: 2028: US-09-107-532A-2028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/592,214A
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2028:
                                               TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                    PLING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 9-UD 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                STREET: SIN Diego CITY: San Diego California
                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yanofsky, Martin F.
RITLE OF INVENTION: Cauliflower Floral Meristem Identify
RITLE OF INVENTION: Genes and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
LENGTH: 4379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 TGATCAGCAAACGAGCAA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7, Application US/08592214A
5811536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 810 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: double
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                        (619)
                                                                                        535-8949
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88.9%;
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                           Version #1.25
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                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/592.
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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OTHER INFORMATION: /note= "N = OTHER INFORMATION: nucleotides.
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                                                                              LOCATION: 2095..2098
OTHER INFORMATION: //
OTHER INFORMATION: ni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Campbell
                                                                                                                                                                                              LENGTH: 4379 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                TELEPHONE:
OTHER INFORMATION:
                             NAME/KEY: misc feature LOCATION: 1..4379
                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                 NAME/KEY: unsure
                                                                                                                                                                  ropology:
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
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1..4379
                                                                                                                                                                                                                                                                  (619) 535-900
(619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1998
                                                                                                                                                                                double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%; Score 14.8; DB 1;
88.9%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                     535-9001
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Genes and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "sequence = Arabidopsis
thaliana AP1 gene"
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 /note= "sequence = Arabidopsis
thaliana AP1 gene"
                                                                                   nucleotides
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                                                                                          /note= "N = one or more
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US-09-103-840A-1
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-103-840A-2
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Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
                             Query Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Patent No. 6294328
                                                                                                     LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
-09-103-840A-1
                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILLNG DATE: 1998-06-24
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis
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TYPE: DNA
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3 GATCGCCAAACGAGCAAC 20
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88.9%;
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88.9%;
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                               0;
                                                 Score 14.8;
Pred. No. 89;
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Pred. No. 1e+02;
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Search completed: February 12, 2004, 06:08:10 Job time: 48.3171 secs

Gaps

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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 218
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                    APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                     / Match 71.0%;
Local Similarity 84.2%;
les 16; Conservative
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                      1 CTGATCGCCAAACGAGCAA 19
CTGATGTCCAAAAGAGCAA 95
                                                                                                                                                                                     FastSEQ for Windows Version 3.0
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Tan, Liqun
Mic
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Fanger, Gary R.
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                                                                                                                                                                                                                                                                                                                                              Samuel X.
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Pred. No. 1.6e
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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
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        published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_
2: /cgn2_6/ptodata/1/pubpna/US06_
3: /cgn2_6/ptodata/1/pubpna/US06_
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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   15 US-10-001-073-15
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10 US-99-878-574-4681
10 US-99-878-574-4681
10 US-99-878-544-0
11 US-09-939-964-1
11 US-09-39-964-1
12 US-10-128-714-1219
15 US-10-128-714-2219
16 US-10-128-714-2219
17 US-10-138-742-2021
18 US-09-938-842A-2021
19 US-09-938-842A-2021
19 US-09-815-242-6644
10 US-10-108-605-116
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Sequence 15, Appl
Sequence 44911, A
Sequence 7065, Ap
Sequence 240, App
Sequence 240, App
Sequence 235, App
Sequence 235, App
Sequence 211, Ap
Sequence 221, Ap
Sequence 2021, Ap
Sequence 2021, Ap
Sequence 2064, Ap
Sequence 26644, Ap
Sequence 116, App
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US-10-138-701-60 US-10-398-221-1962	US-09-070-927A-3	US-10-027-632-173804	-SD		US-09-864-408A-3499	US-10-156-761-1	d	US-10-128-714-380	US-10-398-221-3557	US-09-938-842A-1537	US-09-938-842A-1537	US-10-369-493-45576	US-10-108-260A-936	US-10-369-493-36531	US-10-142-835-29	-10	US-10-036-959B-2	US-10-369-493-31049	US-10-369-493-28292	US-09-983-965-623	US-09-983-965-958	US-09-960-352-5967	US-10-369-493-33107	US-10-369-493-32914	US-10-079-854-216	US-09-764-878-216	US-10-128-714-219	US-10-108-605-324
Sequence 60, Appl Sequence 1962, Ap	ω				Sequence 3499, Ap			Sequence 380, App					936,	365		350,	Sequence 2, Appli	310		623,	958, 1		331	Sequence 32914, A	e 216	Sequence 216, App	219	Sequence 324, App

ALIGNMENTS

Sequence 15, Application US/10001073

Publication No. US20030113725A1

Publicant INFORMATION:

APPLICANT: Liggett, Stephen

APPLICANT: Small, Kirsten

ITITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms

FILE REFERENCE: 13073-PCT

RESULT 1 US-10-001-073-15

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CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-15

Query Match
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 CTGATCGCCAAACGAGCAAC 20
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Db 1 CTGATCGCCAAACGAGCAAC 20
RESULT 2
US-10-369-493-44911/c
Sequence 44911, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NO5: 15775
SEQ ID NO 7065
LENGTH: 277
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701099380H1
US-09-878-574-7065
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 44911
LENGTH: 3325
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; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-44911
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US-09-878-574-7065/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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NUMBER OF SEQ ID NOS:
SEQ ID NO 4681
                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Byrum, C
                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
FURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: US/09/878,574
FRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Byrum, APPLICANT: La Ro APPLICANT: Thomp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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Similarity 89.5%;
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Pred. No.
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Pred. No. 1.3e+02;
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; LOCATION: (1)...(1976)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-039-Q1-B2-G12
US-09-878-574-4681
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US-10-079-854-240
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US-10-079-854-240
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LENGTH: 5786
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                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 240
LENGTH: 5786
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GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
                                                       Matches
                                                                        Best
                                                                                 Query Match
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                                                                                                                                                                                                    Prior Application removed - NUMBER OF SEQ ID NOS: 428
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PA121C1
                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                     Local Similarity
es 17; Conserv
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TTATCGCCAAATGAGCAAC 836
                             TGATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                        Application US/10079854
o. US20030054368A1
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89.5%;
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Pred. No. 1.8e
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Pred. No. 1.6e+02;
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                                                                        Score 15.8;
Pred. No. 1
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                                                                           1.8e+02
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PRIOR APPLICATION NUMBER: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: PASTSEQ for Windows Version 4
SEQ ID NO 235
LENGTH: 705
TYPE: DNA
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US-09-770-149-235/c
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Publication No. US20030054522A1
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                                                                                                                                                                             APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TYPE: DNA
ORGANISM: Rhizobium
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                                       ORGANISM: Arabidopsis thalians
AME/KEY: misc_feature
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es 16; Conserv
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                                                                                                                 FastSEQ for Windows Version 4.0
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Allen, Keith
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Slader, Ted
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matthew, Abranam v
Ledford, Brooke L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An, Yong-Qiang
Hamilton, Carol
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Pred. No. 4.
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; LOCATION: (1)...(705)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-235
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US-10-128-714-2219
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SEQ ID NO 1219
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                                                                                                                                                         APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastlen M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT EPPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
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CURRENT FILING DATE: 2002-04-23
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mes 17; Conserva
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Tishkoff, Danie
Zamudio, Carlos
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85.0%;
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85.0%;
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Pred. No. 3.3e+02
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Pred. No. 3
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RESULT 12
US-09-938-842A-2021/c
US-09-938-842A-2021/c
; Sequence 2021, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2021
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PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR REPLICATION NUMBER: US 60/303,899
PRIOR RELING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: 3001-08-31
NUMBER OF SE0 1D NOS: 8603
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Best Local Similarity
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SEQ ID NO 2021
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LENGTH: 1284
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: US 60/300,111
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                  132 CTCATCGCCAGACGAGCACC 113
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Pred. No. 3.3e+02;
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 206
LENGTH: 2031
TYPE: DNA
ORGANISM: Drosophila melanogaster
                                                                                                     Sequence 6644, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2021
LENGTH: 1359
                                                                                 GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLBIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/761,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
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Bachmann, Jane
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Pred. No. 3.3e+02;
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APPLICANT:

APPLICANT

Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard

APPLICANT

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APPLICANT: Stam, Lynn
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 9/761,142
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: DNA
ORGANISM: Drosophila melanogaster
US-10-108-605-116
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEG ID NOS: 14110
SOPTWARE: PABLESEQ for Windows Version 4.0
SOPTWARE: PABLESEQ for Windows Version 4.0
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ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2193)
US-09-815-242-6644
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US-10-108-605-116
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                               Query Match
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ILE REFERENCE: ELITRA.011A
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783 CCGATCGCCAAACGCCCAAC 802
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                              CTGATCGCCAAACGAGCAAC 20
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85.0%; Pred. No. 3.5e+02;
cive 0; Mismatches 3; Indels 0;
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Pred. No. 3.5e+02;
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Result
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Elkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 275)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.
                                                                                                                                                                                                                                                 BI372571 275 bp mRNA linear EST 01-A RE59566.5prime RE Drosophila melanogaster normalized Embryo Drosophila melanogaster cDNA clone RE59566 5, mRNA sequence. BI372571
  Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                                               Unpublished Contact: St
                                                                      BDGP/HHMI RE Drosophila
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B1946431
B1956836
BH537924
BH6694343
AG071154
BY293513
CCS5449
CS5542
BY284930
BF4512131
BF072723
BF4512131
BF072723
BF45127
BF457549
BF4575663
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              94720,
              USA
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N82961 TgSSTZY53d1
BI946431 DESTRS.5'
BH962262 odg10b08.
BH674374 BOMNUJ43TF
BH56836 BOGYLISTF
BH556336 BOGYLISTF
BH569343 BOHVAA9TF
BH569343 BOHVAA9TF
BH694343 BOHVAA9TF
BH754379 ACBNCOURT
BG255409 AGENCOURT
BG255409 AGENCOURT
BG255789 602366671
AL73862 Tetraodon
BX293513 Arabidops
AL587549 UZ68610.
BH75513 NGLMG0557.
BF46154 MILG0557.
BF46154 BE903605.
AL587075 AL587025
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AL587056 UI-M-BZ1-BU38646 G03860053
BI97437 BA396379 BF457549 UI-M-BZ1-BU38646 G03860053
BI976827 ESTZ71509
BM525002 BA156707.
BM328798 BIC1 26 F
BQ770626 UI-M-F70-BH139984 SZM1-46E16
AQ39921 MSZM003M
BJ122635 BJ122635
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EST 01-AUG-2001 1 Embryo pflc-1

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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
plate: RE.595 row: F column: 6
High quality sequence stop: 246.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thallana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 428)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

2 immerman, J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH756337 428 bp DNA linear GSS SALK 053523.55.75.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 053523.55.75.x,
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    survey sequence.
BH756337
                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from
                                                                                                                                                                                                                                                                                                                                                 Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis Genome 
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH756337.1 GI:19038548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGATCGCCAAACGAGCAA 19
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                                                                                                                                                                                                                                                               TDNA tagged.
                                                                                                                                                                                                                                                                                                                               ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

74 C 67 g 57 t
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/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
/clone_lib="RE Drosophila melanogaster normalized
pFlc-1"
/clone="SALK 053523.55.75.x"
/clone_lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Drosophila melanogaster"

mol_type="mRNA"
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                                                                                                                                 db_xref="taxon:3702"
                                                                                                                                                       'strain="Columbia 0"
                                                                                                                                                                                                organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _xref="taxon:7227"
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94.7%;
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303
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                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 68 row: L column: 5
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UTel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrota
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EST.
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                                                       l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine gene discovery by normalized cDNA-library EST cluster assembly
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CTGATCGACAGACGAGCAAC 322
                           CTGATCGCCAAACGAGCAAC
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                                                                                                                             /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 11, 13, 15, 20 and 30 embryos."

179 c 135 g 117 t
                                                                                                                                                                                                       /mol type="mRNA"
/db xref="taxon:9823"
/tissue type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                          /clone
                                                                                                                                                                                                                                                               organism="Sus scrofa"
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90.0%;
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90.0%;
                                                                                                                                                                                         lib="MARC 1PIG"
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Cetartiodactyla; Suina; Suidae;
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Pred. No. 3.
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3.1e+02;
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Sus.
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BG381314/c
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BG381314 GI:13305786 EST.
                                                                                                                                                                   Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               900 bp mRNA linear EST 23-APR-2001 SD14169.Sprime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD14169 5 similar to CG17509; FBan0017509 located on: 2R 48E2-48E2;: 04/13/2001, mRNA
                                                                                     Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003823: arm:2R [6997351,7260081]
estimated-cyto:48D8-48F5: 04/13/2001
Plate: SD.141 row: F column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvey, D., Brokstein, P., Hong, L., Lewis, S. and Rubin, G.M.
                                   97044477
                                                   Genome Res. 6 (9),
                                                                       discovery
                                                                                                                                                 Rattue.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDGP/HHMI Drosophila EST Project
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                                                                                                                             (bases 1 to 359)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pOT2; Site 1: EcoRI; Site 2: Xho1; Sized fractionated CDNAs were directly ligated into pOT2. Plasmid cDNA library."
186 c 173 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture pOT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Drosophila melanogaster"
|mol_type="mRNA"
|db_xref="texon:7227"
|clone="SD14169"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%;
90.0%;
                                                     791-806 (1996)
                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8; DB 10
Pred. No. 3.7e+02;
0; Mismatches 2
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                                                                                         facilitate
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N82961
LOCUS
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Best Local
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T9ESTZy53d12.r1 TGRH Tachyzoite cDNA Toxoplasma
tgzy53d12.r1 5', mRNA sequence.
N82061
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Fax: 319 335 9565
Email: hemro
Contact: Marra M
WashU-Merck EST Project
Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA sequence:
73-206, >RSIME1#SINE/B4(B5)
                                                                                                                                                                                Hehl, A., Manger, I., Marra, M., Sibley, L.D., Dietrich, N., Dubuque, T., Hillier, L., Kuc. Waterston, R.H. and Boothroyd, J. WashU-Merck-Stanford-NIH Toxoplasma EST pr
                                                                                                                                                                                                                                                                                                                           Sarcocystidae; Toxoplasma.

1 (bases 1 to 477)
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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Toxoplasma gondii
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                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N82961.1 GI:1258714
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//dev stage="ADULT"
//dev stage="ADULT"
//lab_host="Ul-R-CT0" (Pharmacia) with a modified
//clone_lib="Ul-R-CT0" (Pharmacia) with a modified
//note="Vector: pT73D-Pac (Pharmacia) with a modified
//note-pT73D-Pac (Pharmacia) with a modified
//note-pT73D-Pac (Pharmacia) with a modified
//note-pT73D-P
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/db_xref="taxon:10116"
/clone="UI-R-CT0-bui-g-04-0-UI"
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/mol_type="mRNA"
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94.4%;
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Pred. No. 4.7e+02;
0; Mismatches 1;
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       School of Medicine vay, Box 8501, St.
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                                                                                                                                                                                                                                                         Kucaba, T.,
       Louis, MO 63108
                                                                                                                                                                                                                                                             Ajioka, J.A., Asi
aba, T., Wan, K.L.
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SOURCE
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BI946431
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Seq primer: T3
High quality sequence
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17; Conserv
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Kucharski, R. and Maleszka, R.

Kucharski, R. and Maleszka, R.

Evaluation of differential gene expression during development in the honeybee using microarrays and Genome Biol. 3 (2), research0007.1-9 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apis mellifera (honeybee)
Apis mellifera
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bEST28.5' Honeybee brain
                                                                                                                                                                                                                                         Biology Pl., Camberra
Tel: +61 2 6125 0451
Fax: +61 2 6125 3784
                                                                                                                                                                                                                                                                                                                                    Visual Sciences Group
Research School of Biological Sciences, Australian National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI946431.1 GI:16285097
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                                                                                                                                                                                                  Seq
                                                                                                                                                                                                                                                                                                                                                                             Contact: Maleszka R
                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: bEST28.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apidae; Apis.
                                                                                                                                                                                                                                                                                                               University
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Location/Qualifiers
                                                                                                                                                                             primer: M13 reverse.
   Location/Qualifiers
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//clone="tgzy53d12:r1"
//lab host="XL1-Blue MRF'"
//lab host="XL1-Blue MRF'"
//clone_lib="TgRH Tachyzoite cDNA"
//clone_lib="TgRH Tachyzoite Swere grown in human
Toxoplasma RH strain tachyzoites were grown in human
Toxoplasma RH strain tachyzoites were grown in human
foreskin fibroblast cultures in vitro. The library was
constructed by K.L. Wan, Cambridge University. cDNAs were
synthesized from polyA RNAs by oligo d(T) priming and
directionally cloned into the EcoRI to XhoI sites of the
Lambda ZapII vector using the ZAP-cDNA synthesis kit
(Stratagene). WARNING: the library contains a small
(Stratage of cDNAs derived from the human host cells."

percentage of cDNAs derived from the human host cells."
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                                                                                                                                                                                                                       maleszka@rsbs.anu.edu.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Toxoplasma
mol_type="mRNA"
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/dev_stage="adult worker"
                  /tissue_type="central brain,
, deuterocerebrum"
                                                                                                                               organism="Apis mellifera"/
                                                                   sex="female"
                                                                                       db_xref="taxon:7460"
                                                                                                                                                           .594
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                                                                                                               type="mRNA"
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Pred. No. 5.2e+02;
M4 smatches 1;
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                                              mushroom bodies, central body
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R.,
,W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea
Unpublished
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH962262 700 bp DNA 1 odg10b08.b1 B.oleracea002 Brassica oleracea
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High quality sequence stop: 541
Location/Qualifiers
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg10 row: b column: 08
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                                                                             l Similarity
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    TGTTCGCCAAACGAGCAA 239
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/clone lib="Honeybee brain cDNA library"
/note="Organ: brain; Vector: pBluescript II SK-; Site_1:
/note="Organ: brain; Vector: pBluescript II SK-; Site_1:
EcoRI; Site_2: XhoI; cDNA-harboring phagemids were
cobtained by performing mass excission procedure on honeybee
brain cDNA lambda Unizap XR library (Ebert P.R. et al.,
1998, Insect Mol. Biol. 7(2):151-62)."

1932 c 184 g 117 t
                                                                                                                                                                       /clone lib="Boleracea002"
/clone lib="Boleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from /note="Tector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prepusing Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                  /organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
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94.4%;
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Pred. No. 5.7e+02;
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                                                                                                  Score 16.4; DB :
Pred. No. 6e+02;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665
             9712 Medical Center Drive, R
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tlgr.org
DNA is from a doubled haploi
Seq primer: TF
                                                                                                                                                                               Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 765)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea
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Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 749)
1 (bases 1 to 749)
1 (bases 1 to 749)
1 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                         Whole genome shotgun sequencing Unpublished Other GSSs: BOGYI38TR Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                   BH568386
BOGYI38TF BOGY Brassica
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17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-3523
Fax: 301-838-0208
Email: cdcown@tigr.org
DNA is from a doubled haploid provided
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BH674374
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Class: sheared ends.
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ilarity 94.4%;
Conservative
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" a 190 c 191 g 214 t
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/clone="BOMNJ43"
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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Pred. No. 6.2e+02;
0; Mismatches 1;
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lone BOGYI38, genomic
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1 (bases 1 to 794)

1 (bases 1 to 794)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished
Other GSSs: BOGGE84TF
                         N
                                                    l Similarity
17; Conserv
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BOGGE84TR BOGG Brassica oleracea
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                                                                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                              Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chris Town
TGTTCGCCAAACGAGCAA
                         TGATCGCCAAACGAGCAA
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                                                                                                                   /clone_lib="BOGG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
221 c 170 g 162 t
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/note="Vector: pHOS1; Site 1: BstXI; 2
genomic DNA inserted into pHOS1 using
a 161 c 225 g 221 t
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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/clone="BOGGE84"
                                                                                                                                                                                                     'mol_type="genomic DNA"
'strain="TO1000DH3"
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/clone="BOGYI38"
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                                                   Score 16.4; DB 28;
Pred. No. 6.3e+02;
0; Mismatches 1;
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RESULT 12 BH694343/c

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1 (bases 1 to 806)

1 (bases 1 to 806)

1 (bases 1, Utterback, T., Koo, H. and Fraser, C.M.
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Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
Submitted (02-AUG-2001) Asso Fujiyama, Kanagawa 230-0045, Japan
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-23 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-25 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-25 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-26 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-27 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-28 Suehiro-chou, Suehiro-cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes DNA, clone: AG071544
AG071544 1 GI:16623346
                                                                                                                                                                                                                                                                                                                                                                       Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG071544
                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sheared ends.
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/rote="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared force for the phos1 using BstXI linkers"
genomic DNA inserted into PHOS1 using BstXI linkers"
a 167 c 239 g 232 t
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/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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BOHVA49,
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17; Conserv
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IMAGE:6951820 5', mRNA sequence.
CD255409
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LIBRARY
                                                                                                                                                                                                                                                                                                                                                                             Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD255409
CD255409.1 GI:31015875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Daniela S. Gerhard, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLMM14571 row: i column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACGCCAAACGAGCAAC
                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCGCCAAACGAGCAAC 20
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R.Site 2
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/clone_lib="PTB Chimpanzee Male BAC Library"
/s51 c 211 g 23 t 7 others
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/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="PTB-062M08.R"
/clone="IMAGE:6951820"
/dev stage="adult"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="WICHD XGC Brn1"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Sal1; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Prechnologies. Note: This is a Xenopus Gene Collection (XGC)
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                                                                                                                                              /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                   ocation/Qualifiers
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TITLE
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BG253789
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SOURCE
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Search completed: February 12, 2004, 06:05:58 Job time : 1087.71 secs
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519 GATCGCCAAACGAGCAGC 536
                                                                                776 GATCGCCAAACGAACAAC 793
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                  3 GATCGCCAAACGAGCAAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM10299 row: n column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BG253789
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Location/Qualifiers
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/lab_host="NIH_MGC_91"
/clone_lib="NIH_MGC_91"
/note="Organ; prostate; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 226 c 208 g 200 t 1 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4474961"
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seq length: 2000000000
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1: gb ba:*

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3: gb in:*

4: gb om:*

5: gb om:*

6: gb pat:*

7: gb pt:*

9: gb pt:*

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11: gb st:*

12: gb st:*

13: gb un:*

14: gb v:*

13: gb un:*

14: gb v:*

13: gb un:*

16: em fun:*

18: em ow:*

19: em mu:*

10: em ow:*

11: em ph:*

11: em ph:*

12: em ow:*

13: em ph:*

14: em htg hum:*

15: em htg un:*

16: em htg un:*

17: em htg vr::*

18: em htg vr::*

19: em htg vr::*

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20
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
em_htgo_other: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS TITLE JOURNAL	SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION KEYWORDS	RESULT 1 AX350504			43	3 4	4 V	38	37 37			32	30		27	C 25	244	22		19	17		14.		: E 5				oα		c 21	Result No. So
Ligget Alpha-: Patent	Homo sap Homo sap Eukaryot Mammalia	AX350504 Sequence AX350504 AX350504			16.8					16.8	\vdash	17.4	17.4	•	17.4	17.4		17.4		17.4	17.4		18.4	18.4	•		200	200	20	20	2 20	20 20	core
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Small,K.M. c receptor polymorphisms l-A 16 25-OCT-2001;	Chordata; Craniata; Ve Primates; Catarrhini;	20 bp DNA ent WO0179561.		ALIGNMENTS	DRO419811 LCR427254	CPO271336		FCA251174		DSA427263	AC106301	AC116537	AE003485	AC007521	AC116696 AC104510	AC083843	AC017096	AC078903 AF159227	F7H2	AC012972	315	DDAAR2B	BX323232		SSC251177	PVI251176	AF005900	AX548756	AR270618	AX350489	049	AX350504 HUMA2C2	Ü
	ertebrata; Euteleostomi; Hominidae; Homo.	linear PAT 06-FEB-2002			AJ419811 Desmodus AJ427254 Lepus cra	271336	3 01	Felis cat	2525 Elephas ma	NΨ	Rattus	Drosoph	Drosophi	, –	AC116696 Mus muscu AC104510 Drosophil	AC083843 Homo sapi	gap	ACU78903 Homo sapi AF159227 Homo sapi	Sequence	Drosop	15939 Tapirus	947 Dug	BX510991 Danio rer BX323232 Arabidops	40630 Zebrafis	7 Sue ec	51176 Phoca	05900 Homo	AX548756 Sequence	270618 Seq	Sequence	50490 Sequ	AX350504 Sequence M38742 Human alpha	Description

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original source text: Human adult neuroblastoma DNA, clone PCRA2. Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by A.C.Chang, 20-SEP-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990) 91054503
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chang, A.C., Ho, T.F. and Chang, N.C.
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155, Sect II, Li-Noon St.
Taipei, Taiwan, 11221 ROC.
Location/Qualifiers
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/db_xref="GI:177868"
/db_xref="
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/db_xref="taxon:9606"
6 C 3 g
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/db_xref="taxon:9606"
/map="4p16.3-p15"
/clone="PCRA2"
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/gene="ADRA2C"
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_type="neuroblastoma"
ue_type="neural"
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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
Location/Qualifiers
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AX350490
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1344)

Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.

Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization J. Biol. Chem. 276 (7), 4917-4922 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                          2 (bases 1 to 1344)
Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.
Direct Submission
Submitted (26-CCT-2000) Internal Medicine, Universit
Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267,
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
458 c 400 g 26
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 1 from Patent WO0179561
AX350489
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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
Conservative
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Accession Number AF005900; polymorphic sequence lack
three glu residues at this location"
/frequency="Caucasians 0.31; African-Americans 0.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
APQNLELVSLAAADILVATLIIPSLANBLLGYWYFRRTWCEVVLALDVLFCTSSIVH
LCA1SLDRYWAVSRALEYNSKTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPDRB
CRPQCKLNQBAWYILASSIGSFFAPCLIWILVYLRIYLLAKRSNRRGPRAKGGPGGES
KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
458 c 405 g 26
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TLRGQVLLGRGVGA1GGQWWRRRAQLTREKRPTFVLAVVIGVFVVLCWFPFFFSYSLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="G-protein coupled receptor"
/codon_start=1
/product="alpha_2B_adrenergic receptor"
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/db_xref="GI:12698670"
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                                                                                                                                                                                                                                                                                                                                   Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for [1] kindly submitted by J.W.Lomasney, 03-M3X-1990, for release after publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W., Yang-Peng, T.L., Caron, M.G. and Lefkowitz, R.J. Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2

Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
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Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
Location/Qualifiers
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Sequence 1181 from patent
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/codon_start=1
/protein_id="AAA51666.1"
/protein_id="AAA51666.1"
/db_xref="GD1:178198"
/db_xxef="GD8:G00-120-539"
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                                                                                                                                                                          gene="ADRA2B"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 41 from Patent WOO2061087.
AX548756
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Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such
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Homo mapiens alpha2B-adrenergic
complete cds.
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Patent: WO 02061087-A 41 08-AUG-2002;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cayla,C., Schaak,S., Bouloumie,A.,
Alpha2/2-adrenergic receptor gene
Cayla,C., Schaak,S., Bouloumie,A., Devedjian,J.C. Direct Submission Submitted (29-MAY-1997) INSERM Unit 317, Institut CHU Rangueil, Toulouse 31403, France
                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                      Unpublished
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LPNSGQQQKEGVCGASPEDEAEEEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
VLATLRGQVLLGRGVGAIGGQWWRRRAHVTREKKFTFVLAVVIGVFVLCWFPFFFSYS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                      Louis Bugnard,
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AC092603 AC073396
AC092603.2 GI:16303539
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                         4 (bases 1 to 22842)
Waterston,R.H.
Direct Submission
Submitted (20-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MC 21108 "108"
                                                                                                                                                                                                                       Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doebber,A. The sequence of Homo sapiens BAC clone RP11-139J6 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 22842)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Mammalia; Eutheria; Primates;
                                                                                                                  Direct Submission
Submitted (19-JUL-2001) Genome
University School of Medicine,
MO 63108, USA
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Waterston, R.H.
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/product="alpha28-adrenergic receptor"
/product="alpha26258.1"
/protein_id="Abh62558.1"
/protein_id="Abh62558.1"
/db_xref="GI:2245628"
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/tranblation="MDHQDPYSVQATAAIAAAITFILLETIFGNALVILAVLTSRSLR
APQNILFLVSLAAADILVAFILIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVVLIIAKRSNRRGPAKGGPGQGER
RPQCKLNQEAWYILASSIGSFPASACHAEVNGHSKSTGEKEGGFTFEDTGTRALPPSWAA
RPQCKLNQEAWYILASSIGSFPASACHAEVNGHSKSTGEKEGGFPAVPVSPASACSPPLOQPQGSR
LPNSGGQCKEGYCGASPEDEABEEEEEEEEEEEEEDAVPVSPASACSPLOQPQGSR
LATIRGQVILGRGVGAIGGGWWRRAAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYS
LATIRGQVILGRGVGAIGGGWWRRAAQLTREKRFTFUNDFFRAFRRILCRPWTQTAW
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/gene="alpha2C2AR"
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1 2747 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="alpha2C2 adrenergic
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                                                                                                                                             Sequencing Center, Washington 4444 Forest Park Parkway, St.
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TITLE
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Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Oct 20, 2001 this sequence version replaced gi:14916188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 (bases 1 to 22842) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (33-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP11-401C13, 2000 bp overlap; the clone sequenced to the right is RP11-574017, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                  The sequence of AC073396 has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Polymorphisms have been identified between AC013272 and AC092603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ Summary Statistics
Center project name: H_NH0139J06
Drafting Center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
                         /rpt_family="(TG)n"
1424. .1449
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                                                                    /rpt_family="MIR"
1377. .1424
                                                                                                                                                                                                    /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                           'map="2"
                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                               Location/
                                                                                                                                    clone_lib="RPCI-11"
                                                                                                                                                           clone="RP11-139J6"
    _family="(GA)n"
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/note="similar to
(NID:g12933576)"
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/note="similar to
(NID:g12886265)"
                                                                                                                         15084. .15487
/note="similar to Sus scrofa EST AW785035 (NID:g7841811)"
                                                                                                                                                                                                                                                                                                                                  /rpt_tamily="
14762. .14822
                                           (NID: 98082456)"
                                                                                                               15110. .15648
                                                                                                                                                                         /note="similar to (NID:g12877089)"
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                                                                                         'note="similar to
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                                                                                                                                                                                                                                                                                    note="similar to Homo (NID:g12877089)"
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                         family="G-rich"
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                                                                                         Rattus
                                                                                                                                                                                                  Homo sapiens EST AL544609
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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aar2B gene; alpha adrenergic receptor 2B.
Phoca vitulina (harbor seal)
Phoca vitulina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVI251176 1168 bp DNA linear MAM 01-JUN-2
Phoca vitulina partial aar2B gene for alpha adrenergic receptor
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Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
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LASSIGSFRAPCLIMILVYLRIYLIAKUSHPRGPGAKGGPGESKOPRSVPTGTSTK
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PEEEABEEEEEEECEPQALPASPASACSPPLPOPOGSRVLATLRGQVLLGRGVGTAS
GQWWRRRAAGLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
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/note="match to EST AA836522
a 7173 C 6248 g 4624 t
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20537. .20973
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22057. .22471
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20027. .20223
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19266. .19675
                                                                                                                                                                                                                                                                           'gene="aar2B"
                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:9720"
                                                                                                                                                                                                                                                                                                                                                                           organism="Phoca vitulina"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                  'gene="aar2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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Parallel adaptive radiations in two major clades of placental
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Sus scrofa (pig)
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AJ251177
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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21082081
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SSGQWWRRAQGLTREKKRTFVLAVVIGVFVLCWFPFFFSYSLGALCPQHCKVPHGLF"
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/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="aar2B"
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sp. partial A2AB gene for alpha
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                     linear ROD 25-OCT-200
2B adrenergic receptor,
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AJ427259:1 GI:21655549

AJ427259:1 GJ:21655549

A2AB gene; alpha 2B adrenergic receptor.

Anomalurus sp.

Anomalurus gp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Anomaluridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences de l'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huchon, D., Madsen, O., Sibbald, M.J., Ament, K., Stanhope, M.J., Catzeflis, F., de Jong, W.W. and Douzery, E.J.
Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes
Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                                                                                                                      complete sequence.
AL840630
AL840630.15 GI:31071445
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
1 (bases 1 to 149169)
                                                                                                                                                                                                                                                                         AL840630
Zebrafish DNA sequence
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Douzery, E.J.P.
                                                                                                            Danio rerio
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                                                                                                                                   Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGACGCCAATGACCACAG 1082
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/number=1
a 391 c
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/
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Pred. No. 72;
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                                                                                                                                                                                                                                                                                                  149169 bp
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CH211-279L11 in linkage group 17,
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REFERENCE
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TITLE
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VERSION
KEYWORDS
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BX510991/c
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TITLE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNT
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Query Match
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: RMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21021
                                                                                                                                                                                                                                                                  171406
Danio rerio clone RP71-44C4,
unordered pieces.
BX510991
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Submitted (24-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on May 23, 2003 this sequence version replaced gi:30722485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                          Sims,
                                                                     Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                             BX510991.3 GI:31071389
HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-279L11_is_from_a_CHORT-211_BAC_library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: pTARBAC2.1
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                                                    (bases 1 to 171406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="CHORI-211"
26273 c 26492 g 48515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18.4; DB 5;
Pred. No. 1.2e+02;
0; Mismatches 1,
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                                                                                                                                                                                                                                                                                                                               SEQUENCING
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                                                                                                     Vertebrata; Euteleostomi; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 149169;
                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                            linear HTG
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JOURNAL

Submitted (21-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,

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COMMENT
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 167404 bases at least Q40
Consensus quality: 168324 bases at least Q30
Consensus quality: 168918 bases at least Q20
Insert size: 170706; sum-of-contigs
Insert size: 169513; 3.5% error; agarose-fp
Quality coverage: 7.49x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 23, 2003 this sequence version replaced gi:30962299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coverage: 7.55x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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164115
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56670
62068
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fragment_cuc
7577, 154106
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62168. .88720
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                                                                                                                                                                                                                                                                                                                                                               vector_side:left"
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                                                                                                  note="assembly_fragment:01032
ragment_chain:1"
                                                                                                                                                                                                                                            note="assembly_fragment:02082
ragment_chain:1"
                                                                                                                                                                                                                                                                                                                  note="assembly_fragment:00525
ragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-71"
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56699: gap of 100 bp
62067: contig of 5398 bp in length
62167: gap of 100 bp
88720: contig of 26553 bp in length
88820: gap of 100 bp
134708: contig of 45888 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one="RP71-44C4"
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14: gap of 100 bp
06: contig of 7192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of 100 bp
contig of 7668 bp in length
gap of 100 bp
contig of 11530 bp in length
gap of 100 bp
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BASE COUNT
ORIGIN
片
                     S
                                                 Matches
                                                             Query Match
Best Local Similarity
                                                                                                                                                                            misc_feature
33134
                        1 AAAAACGCCAATGACCACAG 20
AAAAACACCAATGACCACAG 33115
                                                                                                                57035 a
                                                 Conservative
                                                                                                                                    /note="assembly fragment:00689
fragment chain:1
clone_end:SP6
                                                                                                                                                                            /note="assembly_fragment:00067
fragment_chain:1"
164215 171406
                                                                                                              ecto\overline{r} side:right" 29367 c 29252 g
                                                             92.0%;
                                                Score 18.4; DB 2;
Pred. No. 1.2e+02;
0; Mismatches 1;
                                                                                                                55051 t
                                                                                                                701 others
                                                                         Length 171406;
                                                  0;
                                                  Gaps
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0,

Search completed: February 12, 2004, 04:41:51 Job time : 589.854 secs

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Result
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                       88
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                                                                                                                              Query
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Gapop 10.0 , Gapext 1.0
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MOVOLOGO	מבור מונים מ	ABV14159	ABV12301	ABV10915	ABV10894	ABV10857	ABV10837	ABV10828	ABV10804	ABV10712	ABV10681	ABV10659	ABV10656	ABV04990	ABV01746	ABV01725	ABV01635	ABV01543	ABV01490	ABV01487	ABV40901			ABA03041							AAT48442	AAT48444	ABL03674	ABN98529	ABZ42624	ACA56583	AAT59499
numan prostate exp		prostate															prostate	prostate	prostate	prostate	Human prostate exp	Human prostate exp	Listeria monocytog	Listeria monocytog	C glutamicum codin	Listeria monocytog	C glutamicum codin	Listeria monocytog		Human TGF-beta-lik	Human TGF-beta-lik	Human TGF-beta-lik	Drosophila melanog	Arabidopsis thalia	Human alpha 2b-adr	Human signalling p	Human alpha-2b adr

ALIGNMENTS

AAI99910 standard; DNA; 20

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RESULT 1
AA19910
ID AA199
XX AA19
XX AA19
XX AA19
XX Huma
XX Huma
XX Huma
XX Huma
XX Homo
XX H
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Liggett SB,
                                                                                                                                                                                                                                         17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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                                                                                           (LIGG/) LIGGETT S.B. (SMAL/) SMALL K M.
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Small KM
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RESULT 2
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                                                                                                                                                                                                                                                                                          norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                        Human, cardiant, gene therapy, alpha2B-adrenoceptor, alpha2B-AR; glutamic acid repeat, intracellular loop, chromosome 2, catecholamine,
                                                                                                                                                                                                                                                                                                                                                                                                                      Human alpha2B-adrenoceptor (alpha2B-AR) variant gene
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llarity 100.0%;
Conservative 0
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/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
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                                                                                                                                                                                                                                                                                              chronic angina 's variant; ds.
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26-APR-2001

WO200179561-A2

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RESULT 3
AA199906 /
AA19999 XX
AC AA1999
XX
BC AA1999
XX
BC AA1999
XX
BC Human
XX
BC Human
XX
BC CENTRA
KW POLymo
KW CENTRA
KW CENTRA
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BC HOMO &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Snapir A,
Scheinin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000; 2000WO-FI00913
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                                                                                                                                                                                Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                                                                                                           Human alpha-2BAR third intracellular loop variant encoding DNA
                                                                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                        AAI99906;
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                                                                                                         Location/Qualifiers
                                /*tag= a
/product= "alpha-2BAR"
/product= "alpha-2BAR"
/note= "sequence is deleted for a 9 nucleotides '
/note= polymorphic site found at nucleotides '
of the wildtype alpha-2BAR protein (AA)
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Nyyssoenen
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RESULT 4
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ID AAD44388 s
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AC AAD44388;
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DT 13-DEC-200
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DE Human alph
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KW Human; hyr
KW hypertensi
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Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the wildtype gene (AAI99905).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
Human; hypertension; alpha-2B-adrenoceptor; AR; hypertension; hypotensive; variant; gene; ds.
                                                                                                13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1344
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                                                        Human alpha-2B-adrenoceptor variant DNA.
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10-AUG-2000;
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SMALL K M.
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; 2000US-0692077.
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                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                          220 A; 458 C; 400
                                                                                                                                                                        DNA; 1344
                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 5.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          <u>د</u>
                                                                                                                                                                                                                                                                                                                                                                                                                            266 T; 0
                                                                                                                                                                                                                                                                                                                                                                5.7;
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                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                    antihypertensive;
                                                                                                                                                                                                                                                                                                                                                                                    Length 1344;
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AAD04762/c
ID AAD047
XX
AC AAD047
XX
AC AAD047
XX
Human
XX
Human;
XW
Human;
XW
Gorona
XW
Corona

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Best Local :
                                                                                                                                                                                                Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2E glutamic acid repeat; intracellular loop; chromosome 2; cate norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                   Human alpha2B-adrenoceptor (alpha2B-AR) gene.
                                                                                                                                                                                                                                                                                                                                                                                                        04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD04762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD04762 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the anthypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 24-26; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200266617-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131
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)B; AAE26633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
/*tag= a
/product=
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human alpha-2B-adrenoceptor variant
protein"
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                                                                                                 Location/Qualifiers
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                          "Human alpha2B-adrenoceptor
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5.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1344;
                                                                                                                                                                                                                                                                            alpha2B-AR;
2; catechol
                       (alpha2B-AR)
                                                                                                                                                                                                                                                                          catecholamine;
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RESULT 6
AA19905/c
ID AA1999
XX AA1999
AC AA1999
AC Human
DE Human
XX Human
XX Human
XX Centr
KW Polymc
KW Polymc
KW Polospl
KW GenBai
XX Homo
XX Homo
XX EFT CDS
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                     В
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                         Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2BAR; GenBank Accession AF009500; chromosome 2; ds.
                                                                                                                                                                                                                Human alpha-2BAR third intracellular loop encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of catecholamines norepinephrine and epinephrine. An antagonist of vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries and a disease involving as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                        18-FEB-2002
                                                                                                                                                                                                                                                                                   AAI99905,
                                                                                                                                                                                                                                                                                                              AA199905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
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Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000; 2000WO-FI00913
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                                                                                                            sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                           standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                              AAAAACGCCAATGACCACAG 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heinonen P, , Salonen JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                   (first entry)
/*tag= a
/product= "alpha-2BAR"
/note= "sequence includes a 9 nucleotide polymorphic
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0422985.
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Pred. No.
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T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB ;
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                                                                                                                                                                                                                   DNA.
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Nyyssoenen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of coronary
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SAXAXE
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AAD44389/c
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                                                                                                                                                                                                                                                                                                                               CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC (b) detecting a polymorphic site comprising apolymorphic polymorphic site comprising of (I), a site comprising cytosine or guanine at positions 901-909 (CC (b) detecting a polymorphic site comprising nucleotide positions 901-909 (CC or a site comprising (Ytosine or guanine at position 753 of (IIV) (CC positions 961-972 of (III). The method may be used for genotyping an expectation yell-972 of (III). The method may be used for genotyping an comprising (A) (9999099900) or (B) (9999090909) at (CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine comprising the alpha2B, alpha2A or alpha2 comprising detecting a cC disease, central nervous system disease and combinations of these. In cC disease, central nervous system disease and combinations of these. In cC disease, central nervous system disease and combinations of these. In cC disease, central nervous system disease and combinations of these. In cC disease, central nervous system disease and combinations of these. In cC disease, central nervous system disease and combinations of these. In cC disease, by detecting the polymorphic site of c.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BH7933 and cC an alpha2B, alpha2A, or alpha2C agonist (e.g. vohimbine, prazosin, ARC 239, cc combinations of these) by detecting the polymorphic site and correlating the site to a cryolase, MAP kinase activity, phosphorylation or inosical phosphate (CC levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR (GenBank Accession AF009500), the sequence includes a pucleotide polymorphic site an uncleotides 901-909, absent in the cCC alpha-2BAR variant (AA199906).
                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 20
           13-DEC-2002
                                              AAD44389;
                                                                                AAD44389
                                                                                                                                                                                                                                                                                                             Sequence 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 144; 163pp; English
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(SMAL/)
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10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                      Similarity
                                                                            standard;
                                                                                                                                                                AAAAACGCCAATGACCACAG 1121
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SMALL K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SB,
                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
       (first entry)
                                                                                                                                                                                                                                                                                                         BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ™ S
                                                                                                                                                                                                                                                                                                       224 A; 458 C;
                                                                          DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at nucleotides 901-909 variant (AAI99906)"
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                              Score 20; DB
Pred. No. 5.7
0; Mismatches
                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                     405 G;
                                                                                                                                                                                                                                                 5.7;
                                                                                                                                                                                                                                                                                                 266 T; 0 other;
                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                              1353;
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                                                                                                                                                                                                                          Gaps
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Human alpha-2B-adrenoceptor gene

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AAQ14151/c
D AAQ14151 standard; DNA; 2064 BP
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                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human
                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a risk of hypertension and targeting treatment in a subject by determining the pattern of alleles encoding a variant alpha-2-adrenoceptor -
01-OCT-1991.
                                                                                                                                                              06-JAN-1992
                                                                                                                                                                                    AAQ14151;
                                                                                                                                                                                                                                                                                                                                                            Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      alpha-28-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 27-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salonen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001FI-0000323
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                     US5053337-A.
                                                                                          Homo
                                                                                                                Neurotransmission;
                                                                                                                                      Human alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-667063/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002; 2002WO-FI00113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive; hypertension; hypotensive; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JURI-) JURILAB LTD OY
                                                                                                                                                                                                                                                                    1140
                                                                                         sapiens
                                                                                                                                                                                                                                                                                          μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE26634.
                                                                                                                                                                                                                                                                                  AAAAACGCCAATGACCACAG 20
                                                                                                                                                                                                                                                                   AAAAACGCCAATGACCACAG 1121
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                             (first entry)
                                                                                                                                      beta
                                          Location/Qualifiers
288..1752
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human alpha-2B-adrenoceptor protein"
                                                                                                               adrenaline;
                                                                                                                                      adrenergic
                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB
100.0%; Pred. No. 5.7;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      gene.
                                                                                                                                      receptor gene
                                                                                                               epinephrine; NGC-alpha2beta; ss
                                                                                                                                                                                                                                                                                                                                       DB 24;
                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                     Length 1353;
                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 9
AAT59499/c
ID AAT594
XX AAT594
XX AAT594
XX DT 06-MAY
XX C AAT594
XX 
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Best Local S
Matches 20
                                                                                                                                                                                                                         30-OCT-1989;
30-MAY-1991;
22-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone NGC-alpha2beta was isolated from a human spleen genomic library by screening with a fragment of the human 5-HT1A receptor gene. The gene can be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine; signal transduction; neurotransmitter; ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT59499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT59499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding alpha, 2-beta adrenergic receptor, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weinshank RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-1989;
                                               WPI; 1997-107576/10.
P-PSDB; AAW11804.
                                                                                                                                                                                                                                                                                                                               22-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alpha-2b adrenergic receptor genomic DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated DNA encoding human adrenergic receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR14149
                                                                                                                        Hartig
                                                                                                                                                                                                                                                                                                                                                                                                                                US5595880-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEUR-) NEUROGENETIC CORP.
                                                                                                                                                                          (SYNA-) SYNAPTIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1991-310087/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                        PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAAAACGCCAATGACCACAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 2064 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAACGCCAATGACCACAG 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                        Weinshank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 319 A; 696 C; 659 G; 390 T; 0
                                                                                                                                                                                                                         89US-0428856.
91US-0707604.
92US-0965040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartig PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89US-0428856
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                                                                                                                                                                                                                                                                                                                               92US-0965040
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288:.1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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0,

Assay for alpha-2b adrenergic receptor ligands - using membranes

0f

cells expressing recombinant receptor

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RESULT 10
ACA56583/c
ID ACA565
XX ACA565
XX ACA565
XX Human
XX Human;
KW signal
KW signal
KW inmunc
XX Homo s
XX Homo s
XX Homo s
XX Homo s
YX US6500
XX US6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                         The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in the diagnosis and treatment of cancer and immunopathology and neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAM1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk-cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and bind to, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-352189/33.
                                                 discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Au - Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACA56583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6500938-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA56583 standard; cDNA; 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenergic receptor. on 25-MAR-2003 to co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                              development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0016434
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                                                                                                                                                                                                                                                                                                                                                      NO 1181;
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                                                                                                                                                                                                                                                                                                                                               65pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                      English
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Disclosure;

invention describes antigenic peptides

comprising

disease

English.

autoimmune diseases Fig 1; 523pp;

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RESULT 11
ABZ42624 s
ID ABZ42624 s
XX ABZ42624 s
AC ABZ426
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Best Local S
Matches 20
                                                                                                                                    New isolated antigenic peptides e.g., for G (GPCR), useful for diagnosing and designing conditions in which GPCRs are involved, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzhelmer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
                                                                                                                                                                                                                                                                                                                                                   Burmer GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, CDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-2000; 2000US-257144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 2001WO-US50107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1552
                                                                                                                                                                                                                                                                                          2003-046718/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                         LIFESPAN BIOSCIENCES
                                                                                                                                                                                                                                                               ABP81780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAACGCCAATGACCACAG 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAACGCCAATGACCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2072 BP; 316 A;
                                                                                                                                                                                                                                                                                                                                                   Rough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypotension; renal
                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                   Brown JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T; 0 other;
                                                                                                                                       protein-coupled receptors.
drugs for treating
   AIDS, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular CC grotein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting antibody against a particular GPCR, and in the production of specific CC antibodies. The peptides and antibodies are also useful for detecting the CC GPCRs and antibodies are also useful for detecting the CC GPCRs and antibodies are useful for detecting the CC greatening immune-related diseases, growth-related cell proliferative CC treating immune-related diseases, growth-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, cell cell seases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, of the control of the protection of the present invention, which are used in the code of inflammation, schizophrenia, dementia, mental retardation, memory content of the control of the present invention, which are used in the cc gramplification of the present invention, which are used in the cc gramplification of the present invention.
 RESULT 12
ABN98529/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN98529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN98529 standard; DNA; 965 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3274 BP;
                              (LEDF/)
                                                             (RAME/)
(PAGE/)
(MATH/)
                                                                                                        (RAIN/)
                                                                                                                                      (PRIC,
                                                                                                                                                   (HAMI/)
                                                                                                                                                                     (GORL/)
                                                                                                                                                                                                                27-JAN-2000; 2000US-178472P
                                                                                                                                                                                                                                                 26-JAN-2001; 2001US-0770445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1140 ANANACGCCAATGACCACAG 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAAAACGCCAATGACCACAG 20
                        RAMEAKA J G.
PAGE A.
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
                                                                                                        HAMILTON C M.
PRICE J L.
RAINES T M.
YU Y.
HAAS W D.
GARCIA C A.
                                                                                                                                                                                   GORLACH J.
                                                                                                                                                                     Ž
                                                                                                                                                                                                                                                                                                                                                                                      crop; thale cress; tolerance factor; insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 A; 979 C; 967 G; 741 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB
Pred. No. 6.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3274;
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                                                                                                                                                                                                                                                                                                                                                                                    pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                   297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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ABL03674

ABL03674 standard; cDNA;

4910

ВP

밁 S

219

2 AAAACGCCAATGACCACAG 20

Matches Best Query Match

18;

Conservative

0; Mismatches Pred. No. Score 17.4;

95; DB 24;

Length

965; 0

Gaps

0

Local

Similarity

87.0%; 94.7%;

Sequence 965 BP; 218 A; 314 C; 161 G; 268 T; 4 other;

ecification, but was obtained in electronic format d seqdata.uspto.gov/sequence.html?DocID=999909770445.

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CC comprising a sequence capable of hybridising under stringent conditions CC comprising a sequence selected from any one of 999 sequences (ABN99231). CC given in the specification or its fragment. A polypeptide (II) encoded by CC (II), a transgenic plant (III) comprising an exogenous nucleic acid, is cC useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded CC useful in identifying homologous or related genes, in producing CC compositions that modulate the expression or function of its encoded CC protein, mapping functional regions of the protein and in studying secreening assays of various plant strains to determine the strains that CC are best capable of withstanding a particularly plant cells. (I) is also useful in Screening assays of various plant strains to determine the strains that CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC pathways. The screened agents are useful in improved methods of treating crops to programs to identify agents that mimic or enhance the action of tolerance of enhance their tolerance to environmental stress. (I) is also useful in a local content to which cc expression of proteins of interest, for establishing the extent to which cc elucidation content function of the manual for screening compounds to 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorlach J,
Rameaka JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 297; 49pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-400781/43.
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Hurban P;
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(SLAT/)
(DAVI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An Y, Hamilton CM,
Page A, Mathew AV,
Kricker M, Slater T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Price JL, Raines TM,
Ledford BL, Woessne,
Davis KR, Allen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woessner JP,
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RESULT 14
AAT48444/c
ID AAT484
XX AAT484
XX III-APF
XX PCLL3
KW Immuni
KW wound
KW wound
KW autoi
XX
OS Homo
XX
FH Key
FT CDS
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                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detection reagent useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                    pCL13; clone 13; transforming growth factor-beta; TGP-beta; immunosuppressive; cell differentiation; antiproliferative; wound healing; vulnerary; ischaemic injury; inflammation; eautoimmune disease; fibrotic disease; diagnosis; gene thera
                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published pct sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5504; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene; ss.
                                                                                                                                                                                11-APR-1997
                                                                                                                                                                                                                                   AAT48444 standard; cDNA; 1441
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4910 BP; 1279 A; 1083 C; 1134 G; 1414 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-656860/75.
DB; ABB59571.
                                                           sapiens
                                                                                                                                                   TGF-beta-like cytokine pCL13 variant u2.
                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                            1 AAAAACGCCAATGACCACA 19
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                     AAAAACGCTAATGACCACA 2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                              (first entry)
                   Location/Qualifiers 234..1160
                                                                                                                                                                                                                                                                                                                                                                87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 17.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                    Pred.
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                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                   .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                               Length 4910;
                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5504.
                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 15
AAT48442/c
ID AAT484
XX AAT484
AC AAT484
AC AAT484
XX Y
DT 11-APR
XX PCL13;
XW immunoo
KW immunoo
KW wound i
KW autoim
XX wound s
XX Homo s
XX Wo9700
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22-JUN-1995;
23-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variants of clone 13 (AAT48438), which codes for pCL13 (AAW10662), a novel TGF-beta-like cytokine whose activities include immunosuppression, down-regulation of leucocyte extravasation and motility, promotion of cell differentiation and inhibition of proliferation. The clones were obtd. from a foetal lung library using a portion of the coding region of clone 13 (see also AAT48438) using a portion of the coding region of clone 13 (see also AAT48438) probe. They show substantial variation in the 5' untranslated region but following statements.
                                                                                                                                             pCL13; clone 13; transforming growth factor-beta; TGF-beta; immunosuppressive; cell differentiation; antiproliferative; wound healing; vulnerary; ischaemic injury; inflammation; cautoimmune disease; fibrotic disease; diagnosis; gene thera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region but only minor differences in the coding region. Translatucoding regions are given in AAW10666-73. While the variants may limportant in e.g. transcriptional reglation they are untranslated and hence cannot affect bloactivity.
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                                                                                                                                                                                                                                                                                          AAT48442
                                                                                                                                                                                                                                                                                                                      AAT48442 standard; cDNA; 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1441 BP; 300 A; 451 C; 428 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 17; Fig 20A; 73pp; English
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                                                                                                               Homo sapiens
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                                               Location/Qualifiers 993..1919 /*tag= a
                                                                                                                                                                                                                          cytokine pCL13 variant
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Matches 18; Conserv
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22-JUN-1995;
23-AUG-1995;
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                                                                                                                                                                                                                       Sequence 2177 BP; 462 A; 645 C; 609 G; 461 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 17; Fig 20A; 73pp; English.
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                                                                                                                                              84.0%; Score 16.8; DB 18; Length 2177; llarity 90.0%; Pred. No. 2e+02; Conservative 0; Mismatches 2; Indels 0;
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| cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-09-813-133A-3
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             Sequence 1181, Ap
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Sequence 103, App
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		Sequence 7, Appli	Sequence 157, A	Sequence 3178, Ap	Sequence 4, Appli	Sequence 4, App	Sequence 1188,	Sequence 2780, Ap	Sequence 937, App	Sequence 12, App	Sequence 2684, Ap	Sequence 2032,	Sequence 885, App	•		Sequence 1872, Ap	Sequence 8, App	Sequence 8, App	Sequence 8, Appli	

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Query Match Best Local Similarity	; STRANDEDNESS: 8i TOPOLOGY: linear ; IMMEDIATE SOURCE: ; LIERARY: GENBANK ; CLONE: 9178197 US-09-016-434-1181	(650) R SEQ RACTED	NAME: Zeller, Karen J. REGISTRATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1855-0555	7408B	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA: APPLICATION MOMBER: US/09/0 FILING DATE: HEREWITH	PATENT NO. 6500938 GENERAL INFORMATION: APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: PATHWAY GENE EXF NUMBER OF SEQUENCES: 1490 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA	<pre>bo-09-016-434-1101/C ; Sequence 1181, Application US/09016434</pre>
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               GENERAL INFORMATION:
APPLICANT: LYTH DOUGETTE-Stamm et al
APPLICANT: LYTH DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                              Sequence 1673, Application US/09134001C Patent No. 6380370
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   CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: GATES, EDWARD R.

REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: C00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
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HYPOTHETICAL: N
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TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: doub
TOPOLOGY: circular
MOLECULE TYPE: DNA (
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CLASSIFICATION:
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600 ATLANTIC AVENUE
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NUMBER: US/09/134,001C
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                                                                                                                                                                                                                                                                                 Score 16;
; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Acinetobacter baumannii
US-09-328-352-312
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09029213B Patent No. 6180098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 312
LENGTH: 1779
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SEQ ID NO 1673
LENGTH: 1593
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                           TITLE OF INVENTION: REGULITIES OF INVENTION: EXINUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                       COUNTRY:
CLASSIFICATION:
              APPLICATION NUMBER: US/0 FILING DATE: 31-AUG-1998
                                                                                                                                                                                             STATE:
                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                          District of Columbia
                                                                                                                                                                                                                           600 13th Street,
                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                    CHRISTIAN, Peter D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.0%; ilarity 85.0%; Conservative
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85.0%;
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Pred. No. 1.4e+02;
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Pred. No. 1.
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ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

REGISTRATION NUMBER: 41,425 REFERENCE/DOCKET NUMBER: 50

50179-048

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US-08-931-999-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             squence 4, Application US/08931999 stent No. 6043219
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: FEATURE:
                                                                                                                                                                                                                                                        APPLICANT: Iandolo, John J.
APPLICANT: Crupper, Scott S
TITLE OF INVENTION: Broad S
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5820 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                           ADDRESSEE: Hovey, Williams, T. STREET: 2405 Grand Boulevard, CITY: Kansas City
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LOCATION:
                            FILING DATE:
CLASSIFICATION:
                                                          APPLICATION NUMBER:
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Y: U.S.A.
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1388..1973
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                                                                                                                                                                                                                                                                       Broad Spectrum Chemotherapeutic
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85.0%;
 US 08/710,561
                                                        US/08/931,999
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Pred. No. 1.7e
0; Mismatches
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d, Suite 400
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; SEQ ID NO 3; LENGTH: 55827; TYPE: DNA; ORGANISM: Human US-09-813-133A-3
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Matches
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Matches
                                                                                                                                         Sequence 103, Application US/09177650 Patent No. 6413719
GENERAL INFORMATION:
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Patent No. 6455294
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ISOLATED HUMAN PROTEASE TITLE OF INVENTION: NUCLEIC ACID MOLECULES TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/813,133A CURRENT FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: CL001173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
CURRENT APPLICATION NUMBER: US/09/177,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GAN, Weiniu et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pair
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ATTORNEY/AGENT INFORMATION:
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mes 17; Conserv
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17; Conserv
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85.0%;
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Pred. No. 2.5e+02;
0; Mismatches 3;
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Pred. No. 1.8e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS, ENCODING HUMAN PROTEASE PROTEINS,
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-221-298-106
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; ORGANISM: Homo sapiens
US-09-177-650-103
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NAME/KEY: modified_base
LOCATION: (18)
OTHER_INFORMATION: Where n
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EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 103
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Patent No. 6284241
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Best Local Similarity
                    NAME/KEY: modified_base
                                           LOCATION: (219)
OTHER INFORMATION: Where
                                                                NAME/KEY: modified_base
 OTHER INFORMATION: Where
                                                                                                              NAME/KEY: modified_base
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                                                                                                                                                                                 LOCATION: (129)
OTHER INFORMATION: Where
                                                                                                                                                                                                     NAME/KEY: modified_base
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OTHER INFORMATION: Where n
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OTHER INFORMATION: Where n
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                     NAME/KEY: modified_base
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RESULT 11
US-08-169-715-1/c
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; LOCATION: 264, 286
; OTHER INFORMATION: a,
US-09-313-294A-6186
                                GENERAL INFORMATION:

APPLICANT: Irvine, Bruce D.

APPLICANT: Horn, Thomas

APPLICANT: Chang, Chu-An

APPLICANT: Chang, Chu-An

ITILE OF INVENTION: HIV PROBE

TITLE OF INVENTION: SANDWICH

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:
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SOFTWARE: PEKE
SEQ ID NO 6186
"ENGTH: 291
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                                                                                                                                                   Sequence 1, Application US/08169715 Patent No. 6300056
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APPLICANT:
APPLICANT:
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Patent No. 6476212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ito, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US

CURRENT FAPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SOFTWARE: PERL Program
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 29
TYPE: DNA
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NAME/KEY: modified_base

TOTATION: (255)

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NAME/KEY: modified_base
LOCATION: (250)
OTHER INFORMATION: where n
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OTHER INFORMATION: Where n is
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                STREET:
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SSEE: Morrison & Foerster
F: 545 Middlefield Road, Suite
Menlo Park
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                                                                                                                                                                                                                                                                                                       Similarity
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                                                   HIV PROBES FOR USE IN SOLUTION SANDWICH HYBRIDIZATION ASSAYS
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88.9%;
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Pred. No. 1.6e
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

94025

California

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US-09-661-596A-76/c
; Sequence 76, Application US/09661596A
; Patent No. 6528066
                                                                                                                                           8
                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                   ; TYPE: DNA ; ORGANISM: Acinetobacter baumannii US-09-328-352-3388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-328-352-3388/c
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3388
LENGTH: 1422
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3388, Application US/09328352 Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MONTOY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2230
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
APPLICANT: Grose, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/8 FILING DATE: 18-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,715
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Local Similarity 66.7%;
es 8; Conservarior
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                  INFORMATION:
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16; Conser
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88.9%;
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Pred. No. 2
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Pred. No. 1
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LENGTH: 1788
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                  Patent No. 584409
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/661,596A CURRENT FILING DATE: 2000-09-14 PRIOR APPLICATION NUMBER: US 60/153,779 PRIOR FILING DATE: 1999-09-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Santos, Richard
TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
FILE REFERENCE: 140.0011 0101
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 124884
TYPE: DNA
ORGANISM: Varicella zoster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                              APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Urfer, Roman
TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                             STREET:
                                                                                                        COUNTRY:
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                                                                                         94080
                                                                                                                                            South San
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                                                                                                                                        Francisco
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88.9%;
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Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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Pred. No. 4
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. 3.5e+02;
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CURRENT APPLICATION NUMBER: US/08/359,705B

PILING DATE: 20-Dec-1994

CLASSIFICATION: 424

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/286846

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/215139

PILING DATE: 03/18/94

ATTORNEY/AGENT INFORMATION:

NAME: TO-COCKET NUMBER: 36,700

REFERENCE-DOCKET NUMBER: 90873P2

TELEPHONE: 650/952-9881

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1858 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TO-DOLOGY: Linear

US-08-359-705B-7

Query Match

Dest Local Similarity 93.8%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps

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SACGCAATGACCACAG 20

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Db 1529 ATGCCAATGACCACAG 1514

Search completed: February 12, 2004, 06:08:16
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                               Score
       seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09C PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq2:*

14: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq2:*

15: /cgn2_6/ptodata/1/pubpna/US10B PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10N PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10N PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10N PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10N PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10N PUBCOMB.seq:*
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Match
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Gapop 10.0 , Gapext 1.0
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2072
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US-10-077-870-1
15 US-10-001-073-2
9 US-09-825-923-3
15 US-10-077-870-3
15 US-10-001-073-1
12 US-10-305-720-1181
15 US-10-255-567A-41
9 US-09-770-445-297
12 US-10-369-493-42551
12 US-10-369-493-42551
12 US-10-369-493-42551
12 US-10-369-493-42551
13 US-10-292-798-1745
14 US-10-292-798-1745
15 US-10-017-161-2000
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US-09-825-923-1
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Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1181, Appli
Sequence 41, Appli
Sequence 297, Appl
Sequence 297, Appl
Sequence 4251, A
Sequence 1745, Apple
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15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	16	16	16	16	16	16	16.4	16.4
79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	80.0	80.0	80.0	80.0	80.0	80.0	82.0	82.0
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US-10-312-841-2	US-10-312-841-1	US-10-398-221-2058	US-10-398-221-9	US-10-311-455-980	US-10-225-567A-43	US-09-938-842A-4905	US-09-938-842A-4905	US-10-101-510-450	US-10-001-073-40	US-10-001-073-42	US-10-447-328-31	US-10-369-493-37126	US-10-191-803-211	US-10-027-632-298548	US-10-027-632-298547	US-10-027-632-83957	US-10-027-632-83956	US-10-027-632-298548	US-10-027-632-298547	US-10-027-632-83957	0-027-632	US-10-027-632-156513	US-10-027-632-156512	US-10-027-632-156513	US-10-027-632-156512	US-10-027-632-156514	US-10-027-632-156514	US-09-738-626-1	US-10-398-221-3790
Sequence 2, Appli	ļ,	e 20	9	986	Sequence 43, Appl	4905,		450,		42,	31,	37126						Sequence 298548,	Sequence 298547,	Sequence 83957, A	Sequence 83956, A	Sequence 156513,		_	Sequence 156512,	Sequence 156514,	Sequence 156514,	Sequence 1, Appli	Sequence 3790, Ap

ALIGNMENTS

RESULT 1

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US-10-001-073-16

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Sequence 16, Application US/10001073

PADDICANT: Liggett, Stephen
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: DATE: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-16
Query Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps
OF SEQ ID NO 16
Dest Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps
OF Sequence 1, Application US/09825923
PATENT NO. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Heinomen, Paula
APPLICANT: Karvonen, Matti
APPLICANT: Karvonen, Matki
APPLICANT: Koulu, Markku
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; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1
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US-10-077-870-1/c
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DUA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER: CEC. IN NOC. 10
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
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TYPE: DNA
ORGANIEM: Homo sapiens
FEATURE:
FEATURE:
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
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                                                                                                    Local
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1131 AAAAACGCCAATGACCACAG 1112
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                                      1 AAAAACGCCAATGACCACAG 20
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Salonen, Riitta
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                                                                      100.0%; Score 20; DB milarity 100.0%; Pred. No. 8.4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomi-Pekka
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                                                                                                                     Length 1344;
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RESULT 4 US-10-001-073-2/c

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; LUCATION: (1)..(1350); OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor; OTHER INFORMATION: protein
US-09-825-923-3
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Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
AppLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                                        APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: DATA molecule encoding a variant alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 10:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                   Query Match
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
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APPLICANT:
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                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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1140 AAAAACGCCAATGACCACAG 1121
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                                                                                    Similarity
                           AAAAACGCCAATGACCACAG
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Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
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Alhopuro, Pia
Karvonen, Matti
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Salonen, Riitta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lakka, Timo A
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                                                                 100.0%; llarity 100.0%; Conservative 0
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                                                                                   Score 20;
Pred. No.
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Pred. No.
                                                                    Mismatches
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; TYPE: DNA ; ORGANISM: Homo sapiens US-10-001-073-1
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US-10-001-073-1/c
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                                                                                                 Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukks T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
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APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
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CURRENT FILING DATE: 2002-05-21
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
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100.0%; Pred. No. 8.
tive 0; Mismatches
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; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
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LENGTH: 3274
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Best Local (
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Best Local Similarity
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PRIOR FILING DATE: 2000-12-19
NUMBER OF OTHER PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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NUMBER OF SEQ ID NOS: 2292
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APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
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APPLICANT: Brown, Joseph P.
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ORGANISM: Homo sapiens
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                                                 Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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No. US20030113798A1
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                                                                     Yu, Yang
Rameaka, Joshua G
                                                                                                                                                                                     Hamilton, Carol M. Price, Jennifer L.
                                                                                                                                                                                                                                       Gorlach, Jorn
                                                                                                                     Page, Amy
                                                                                                                                                                     Raines,
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ilarity 100.0%;
Conservative (
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100.0%; Pred. No. 9.1;
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Pred. No. 8.7;
0; Mismatches
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APPLICANT: Hoffman, Neil

APPLICANT: Hurban, Patrick

TITLE OF INVENTION: Expressed Sequences of Arabidopsis

TITLE OF INVENTION: thaliana

FILE REFERENCE: 2023US (PARA-012PRV)

CURRENT APPLICATION NUMBER: US/09/770,445

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: US 60/178,472

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 999

SOFTWARE: FastSFO --

SEO ID NO: FastSFO --
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; LCCATION: (1)...(965)
; OTHER INFORMATION: n = A,T,C
US-09-770-445-297
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                                                     Sequence 1266, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
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SEQ ID NO 42551
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LENGTH: 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Anabaena PCC7120
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1767
                                                                                                                                                                                                                                                                                  Local
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94.7%;
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90.0%;
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Pred. No. 2.8e+02;
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Pred. No. 1
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RESULT 14 US-10-292-798-1745/c

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Sequence 1745, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI

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NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PatentIn ver. 3.0

SEQ ID NO 743

LENGTH: 996
 片
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                                                                                                                                  ; TYPE: DNA ; ORGANISM: Corynebacterium glutamicum US-09-738-626-743
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US-09-738-626-743/c
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; ORGANISM: Listeria monocytogenes-4B
US-10-398-221-1266
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SEQ ID NO 1266
LENGTH: 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 743, Appropriate Publication No.
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
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                                                                                 Similarity
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HAYASHI, MILL.
OCHIAI, KEIKO
OWOI, HARUHIKO
NAOKO
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SENOH, AKIHIRO
IKEDA, MASATO
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                                                                   Conservative
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                                                                                82.0%;
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APPLICANT: SUMA, MAXIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASURATMAN, YUTAKA
APPLICANT: ASURATMAN, TOYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PACENTIN VET. 2.1
SEQ ID NO 2099
LENGTH: 1282
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                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (201)..(1082)
US-10-017-161-2099
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US-10-017-161-2099/c
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; NAME/KEY: CDS
; LOCATION: (201)..(1082)
US-10-292-798-1745
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CURRENT FILING DATE: 0002-11-13
PRIOR APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR PRIOR PRIOR NUMBER: US/10/17,161
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2099, Application US/10017161 Publication No. US20030143668A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.0%; Score 16.4; DB 12; Length 1282; Best Local Similarity 94.4%; Pred. No. 4.2e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                    Query Match 82.0%; Score 16.4; DB 13; Length 1282; Best Local Similarity 94.4%; Pred. No. 4.2e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SOURCE
LOCATION: (1)..(1282)
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE T
                                                                                                                                                                                                                                                                                     FEATURE:
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1071 ACAACGCCAATGACCACA 1054
1071 ACAACGCCAATGACCACA 1054
                               2 AAAACGCCAATGACCACA 19
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Search completed: February 12, 2004, 06:16:00

Job time : 122.659 secs

Mis Pogo Blonk (USO16)

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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18.4
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gb_est2:*
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7748 5	97	ø	670	,	16.4	43
69974 Par	9699	29	655		16.4	42
097 486073C10	Ō	ø	593	۶	16.4	41
99110 947041G0	Ε	12	547	'n	16.4	40
68063 CH240_1	CC468063	29	455	۲		39
G549863	BG549863	10	405	?	16.4	38
9458 1	859	9	355		16.4	37
	BG549263	10	143	۲.	16.4	36
10723 6028	G	12	1336	84.0	٠	35
67326	H	28	1115	4.	٥.	34
40575	BG440575	10	926	4.	٥,	
۳	CNS01MR6	29	916	4.	σ	32
03770	BZ203770	29	896	4.	٥,	31
11552 Tetr	CNS04XDZ	29	889	4	٥.	
606568 Sea	HIPA2C2AR	29	882	4.	٥.	
68763 60305825	BI768763	12	878	4.	٥.	28
	BH270411	28	858	4.	ა	
01034	BQ901034	13	855	4.	٥.	
606584	DREA2CAR	29	788	4.	٥,	25
AZ907242 RPCI-24-1	AZ907242	28	765	4.	σ	24
CB630921 OSIIEb08C	CB630921	14	742	4.	٥.	23
AI055134 coau0003C	AI055134	9	729	4.	ი	22
CB677776 OSJNEe15B	CB677776	14	722		٥.	21
AZ352444 1M0090117	AZ352444	28	. 668	4.		20
BQ109472 imageqc_7	BQ109472	13	658	84.0	٠	19
ST60529	BQ119722	13	635		٥.	18
heg	AZ217526	28	576	Α.	٥.	17
BM690995 UI-E-CI1-	BM690995	12	513		16.8	16
BG143944 ut66h01.x	BG143944	10	500	4	٥,	15
AI243573 qu63c06.x	AI243573	9	445	٠.	٥.	14
AI735704 at2 $\overline{0}$ d01. \overline{x}	AI735704	9	436	4.	٥.	13
AQ432032 HS 2270 A	ű	28	424	4.	٥,	2
BE239439 EST392780	BE239439	10	393	84.0	٥.	F
664	2664	29	321	4.	٠,	0
106085 HS 3054	2	28	241	4.	٥,	9
Z070845 RPCI-23	Z0708	28	179			89
395866 MA000059	395866	9	173		σ.	7
Y030666 BY030666	0306	13				σ
96		10	1752	87.0	17.4	U

ALIGNMENTS

RESULT 1
HGRA2BAR/c
LOCUS
DEFINITION

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

Hexanchus griseus
Hexanchus griseus
Hexanchus griseus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Notidanoidea, Hexanchiformes,

genomic survey sequence.
AL606572
AL606572.1 GI:15591923
GSS; Alpha2 adrenergic receptor gene.

Shark alpha2 adrenergic receptor gene fragment probably subtype b, genomic survey sequence.

AI993504 701496517 AL440137 T3 end of	E788667 BE788667 601475536 source 1712	AL606572 Shark alp FEATURES		Description Centre Hinxton, Ca	JOURNAL Submitted (14-SEP-	TITLE Direct Submission	SUMMARIES AUTHORS Hunter, C.		JOURNAL	ng printed, TITLE	AUTHORS	REFERENCE	Hexanchoidei; Hexa	
/organism="Hexanchus griseus" /mol_type="genomic DNA"			biohelp@hgmp.mrc.ac.uk	Centre Hinxton, Cambridge, CB10 1SB. UK Email:		Direct Submission	ŝ	REFERENCE 2 (bases 1 to 712)			AUTHORS Hunter, C. and Elgar, G.	REFERENCE 1 (bases 1 to 712)	Hexanchoidei; Hexanchidae; Hexanchus.	

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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 986)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BE788667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE788667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
Plate: LLAM9642 row: g column: 10
High quality sequence stop: 254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                               l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                      AI993504 527 bp mRNA linear EST 08-SEP-1701496517 A. thaliana, Ohio State clone set Arabidopsis thaliana cDNA clone 701496517, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
           AI993504
AI993504.1
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                                                                                                                                                                                                                                                               /clone="IMAGE:3878433"
/tissue_type="large_cell_carcinoma"
/lab hose="DH10B (phage_resistant)"
/clone_lib="NIH_MGC_68"
/clone_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Site_2: Sall; Cloned unidirectionally constructed by Life Average insert size 1.8 kb. Library constructed by Life Technologies."

Technologies. "
332 c 157 g 51 t
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                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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187 c 180 g
              GI:5840409
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100.0%;
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Pred. No.
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Pred. No. 2.6e
0; Mismatches
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1.2e+02;
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.6e+02;
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CNS07D83
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                                                                                          REFERENCE
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JOURNAL
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MEDIINE
        JOURNAL MEDLINE
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SOURCE
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Best Local Similarity
Matches 18; Conserv
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Systems, Inc., a wholly owned subsidiary Pharmaceuticals, Inc., 4633 world read
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1 (bases 1 to 527)
tropicalis
FEBS Lett. 487
20584726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: service@genomesystems.com.
Location/Qualifiers
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Candida tropicalis
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS07D83 971 bp DNA linear GSS 08-JU
T3 end of clone BD0AA010C06 of library BD0AA from strain CBS
Candida tropicalis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                          Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
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AL440137.1 GI:12223548
                                                                                                                                                                                                                           Genomic exploration of the hemiascomycetous yeasts: 1. yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                          2 (bases 1 to 971)
Blandin,G., Ozier-Kalogeropoulos,O.,
                                                                              Genomic exploration
                                                                                                                                                                                                              2058471
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314-427-3324
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/note="CDNA library was made from selected clones
Arabidopsis thaliana Ohio State clone set."
163 c 115 g 128 t
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/mol_type="mRNA"
/db_xref="taxon:3702"
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94.7%;
                             (1), 91-94 (2000)
                                                                                 of the hemiascomycetous yeasts: 16. Candida
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Pred. No. 6.4e+02;
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                                                                                                                                  Wincker, P., Artiguenave, F.
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KEYWORDS
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Best Local
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                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM893 row: n column: 16
High quality sequence start: 132
High quality sequence stop: 163.
Location/Qualifiers
                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1752)

NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601811063R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054095 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National
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                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4054095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5482"
/clone="BD0AA010C06"
/clone_lib="BD0AA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
tissue_type="primary B-cells from tonsils (cell line)"
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94.7%;
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Pred. No. 8e+02;
0; Mismatches
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                                                                                                                                                                                                                          Nkadaki, Y., Furno, M., Kasukawa, Y., Adachi, J., Boho, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schrimi, L.M., Kanapin, A., Matsuda, H., Batalov, S., LE., Cousina, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Gough, J., Kanai, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, M., Wang, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, M., Varardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Ring, B.Z., Ringdali, A., Sahaika, Y., Taylor, M.S., Yanagisawa, M., Yang, I., Yang, L., Zavolan, M., Zih, Y., Zimmer, A., M., Yang, I., Yang, L., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, I., Yang, L., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakarume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kayawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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BY030666 RIKEN full-length enriched, 1 cell embryo Mus musculus
cDNA clone IOC0014E12 5', mRNA sequence.
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note: Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
/note: this is a NIH MGC Library."
/note: this is a NIH MGC Library."
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/clone_lib="NIH_MGC_48"
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Pred. No. 9.9e+02;
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   230-0045, Japan
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K. Akimura,T. Arakawa,T. Carninci,P., Fukuda,S., Hirozar
Aizawa,K. Jahii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,f.
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Myazaki,f.
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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AI395866.1 GI:4225413
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MA000059b.FGR Adult worm cDNA emansoni cDNA 5', mRNA sequence.
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Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                              Schistosoma
                                                                                                                                                                                                                                                                                                                                                   Schistosoma mansoni
Tel: 55 31 2953566
Fax: 55 31 2952115
Email: oliveira@netra.cpqrr.fiocruz.br
                                                                                                                                                                                                           Cataloguing Schistosoma mansoni genes with expressed
                                                                                                                                                                                                                                 Oliveira, G.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                  Contact: Oliveira,
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Augusto de Lima 1715 Barro Preto,
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llarity 100.0%;
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/dev stage="1 cell embryo"
/clone_lib="RIKEN full-length enriched,
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/mol_type="mRNA"
/strain="C57BL/6J"
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9.6e+02;
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stosomatidae; Schistosoma
                                                                                                     Belo Horizonte,
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Yazaki,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAAACGCCAATGACCACAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence. AZ070845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao bepartment of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao, S., Nierman, W., Feldblyum, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu) Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resegen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 422 row: G column: 2
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Mouse BAC End Sequences from Library RPCI-23
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1 (bases 1 to 179)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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Class: BAC ends.
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Levins, M., Mcgann, S., Tsegaye, G., Geer, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Bex= "Accument of the manufacturer's instructions."
/ Seve stage="adult"
/ Clone lib="Adult worm cDNA expression library"
/ Clone lib-"Adult worm cDNA expression library"
/ note="Vector: Uni-Zap XR vector, Stratagene (pBluescript / note="Tector: Uni-Zap XR vector, Stratagene (pBluescript / note-English / Stratagene (pBluescript / note-English 
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/strain="LE"
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/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: kidney-Brain; Vector: pBACe3.6; Site_1:
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                    db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                         sex="Female"
                                                                                                                                                                                                                                                                                                                                      clone="RPCI-23-422G2"
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90.0%;
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Pred. No. 8.5e+02;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing primer.
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K., Krol,M.,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 241)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jwallace@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 Queen Anne Avenue North, Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scanning the human genome Proc. Natl. Acad. Sci. U.:
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                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 241.
Location/Qualifiers
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 616-3887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
                                                                                                                                                                                                            /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH108"
54 c 52 g 83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " a 58 c 45 g 0 t
                                                                                                                                                                                                                                                                                                                                                                       1. .241
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                 /clone="Plate=3054 Col=23 Row=I"
                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:3481441
                                                                                                                                                 90.0%;
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Pred. No. 8.6e+02;
                                                                                                                                                 Score 16.8;
Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle,
                                                                                                                                                 5e+02
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RESULT 11
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Best Local S
Matches 18
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BE239439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ664659
321 bp DNA Linear SALK 099680.45.60.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 099680.45.60.x,
                                                                                            Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
. eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L
,Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Harrison,M.J., Town,C.D., Bowman,C.L., Holt,I.E., Cho,J. and Fraser,C.M. ESTs from phosphate-starved roots of Me
                                                                                                                                                                                                                                                                                                                 EST392780 MHRP- Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; core eud: eurosids II; Brassicales; Brassicaceae; Arabidopsis. [ (bases 1 to 321)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ664659.1
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
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                                                                                                                                                                                                    Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 40 c 86 g 104 t
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/mol_type="genomic DNA"
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Pred. No. 1.1e+03;
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    Medicago truncatula
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                                              Craven, M.B., Hansen, T.S.,
                                                                                                                                                                                                                                                                                                                                           linear
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RESULT 12
AQ432032
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                                                                                                                                                         TITLE
                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 424)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.S., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. au
                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ432032

424 bp DNA linear GSS 31-MAR-199
HS 2270 A2 E11 T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2270 Col=22 Row=I, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ
                Contact: Mahairas GG, Wallace JC, Hood High Throughput Sequencing Center
                                                                                                     Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  University
                                                                                         99380589
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             AQ432032.1
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N260974e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          More information is available at. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAACGCCAATGACCACAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=Wector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; At the trifoliate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this period, they were fertilized twice weekly with 1/2 Hoaglands solutions containing 20uM potassium phosphate. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phage using Ex-assist helper phage and propagated in
XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="roots"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
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/cultivar="A17"
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of Washington
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90.0%;
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Pred. No. 1.1e+03;
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KEYWORDS
SOURCE
ORGANISM
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AI735704/c
LOCUS
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ORIGIN
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JOURNAL
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 436)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Wateraton,R. and Wilson,R.
                                                                                                                                                                                                                              High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI735704
436 bp mRNA linear EST 14-JUN-199
at20d01.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2355649 3' similar to gb:MSB458 40S RIBOSOMAL PROTEIN S4, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOFORM (HUMAN);, mRNA sequence.
AI735704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2270 row: I column: 22
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 424.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI735704.1 GI:5057228
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                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-Coli DH10B"
'clone_lib="Barstead aorta מרונה ארשהשט"
note="Organ: aorta; Vector: pT7T3D-Pac (Pharmacia) with
                                                      /dev_stage="adult, age 64"
/lab_host="DH108 (phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2270 Col=22 Row=I"
                                                                                                   'sex="male"
                                                                                                                         clone="IMAGE: 2355649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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Organ: sperm; Vector: pBeloBAC11; BAC Clones i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>,</u>
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 424;
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JOURNAL COMMENT
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AI243573/c
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VERSION
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoo
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TITLE
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                                                                 Matches
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                                                                                Local Similarity
208
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                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI243573 445 bp mRNA linear EST 04-NOV-1998 qu63c06.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1976746 3's similar to gb:M58458 40S RIBOSOMAL PROTEIN S4, X ISOFORM (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 445)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI243573
AI243573.1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown library type
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CGAP/BTGAP), Tumor Gene Index
AAAAATGCCAATGACAACAG 189
                              AAAAACGCCAATGACCACAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAACGCCAATGACCACAG
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                                                                                                                                                105
                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 1.
Location/Qualifiers
                                                               Conservative
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                                                                                                                                  /clone lib="NCI CGAP Brn35"
/clone lib="NCI CGAP Brn35"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall;
/site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
a 85 c 92 g 162 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barstead.
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1976746"
                                                                                                                                                                                                                                                                             /tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:3838970
                                                                                                                                                                                                                                                                                                                                                                                    .445
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90.0%;
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Pred. No. 1.2e+03;
                                                                               Score 16.8;
Pred. No. 1.
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Search completed: February 12,

2004, 06:06:09

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RESULT 15

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AUTHORS
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Matches 18
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                                                                              Local Similarity
320 AAAACAGCCAATGACCACAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 bp ut66h01.x1 Soares mouse NMGB bcell IMAGS:3332976 3', mRNA sequence. BG143944 BG143944.1 GI:12647344 EST.
                             1 AAAAACGCCAATGACCACAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other ESTs. ut66h01.yl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This_clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 480.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE Consortium (info@image.llnl.gov)
MGI:1077140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 500)
                                                                                                                                                 169
                                                                 Conservative
                                                                                                                                           T 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3332976"
                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                              ab_host="DH10B (phage-resistant)"
                                                                             84.0%;
                                                               Score 16.8; 1
Pred. No. 1.20
0; Mismatches
                                                                              .2e+03;
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                                                                                              Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further information
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                                                                 Indels
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